[illegible] version [illegible]
Copyright (c) [illegible] Ltd.

[illegible] search, using sw model

[illegible] Search time [illegible] Seconds
(without alignments)
[illegible] Million cell updates/sec

[illegible] US-10-006-430-76
[illegible]
[illegible]

[illegible] IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

[illegible] residues

[illegible] parameters: [illegible]

[illegible] length: [illegible]
[illegible] length: [illegible]

[illegible] Minimum Match [illegible]
Maximum Match 100%
Listing first 45 summaries

[illegible] GenEmbl:*
[illegible] gb_ba:*
[illegible] gb_htg:*
[illegible] gb_in:*
[illegible] gb_om:*
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[illegible] em_htgo_mus:*
[illegible] em_htgo_other:*

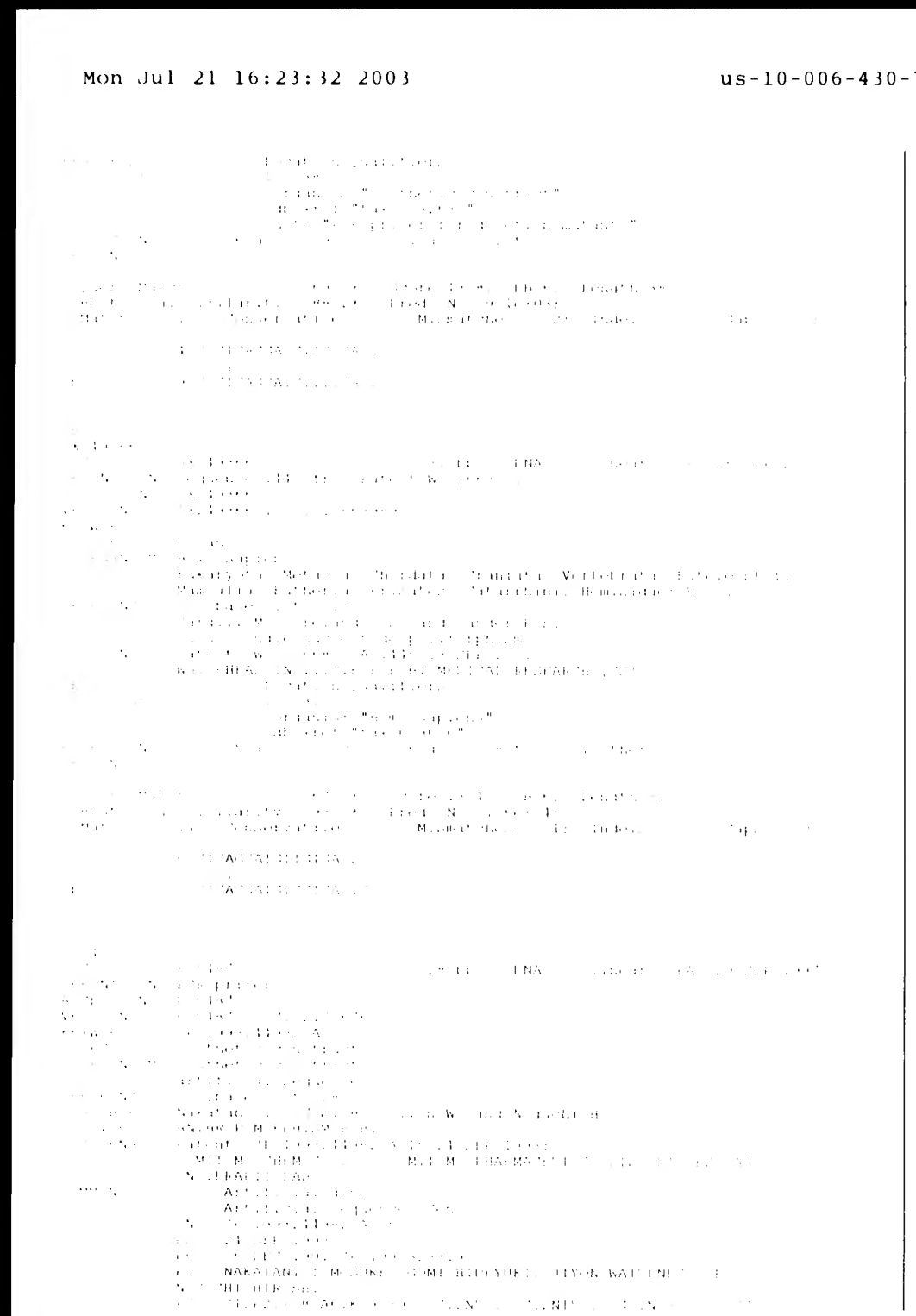
[illegible] The number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

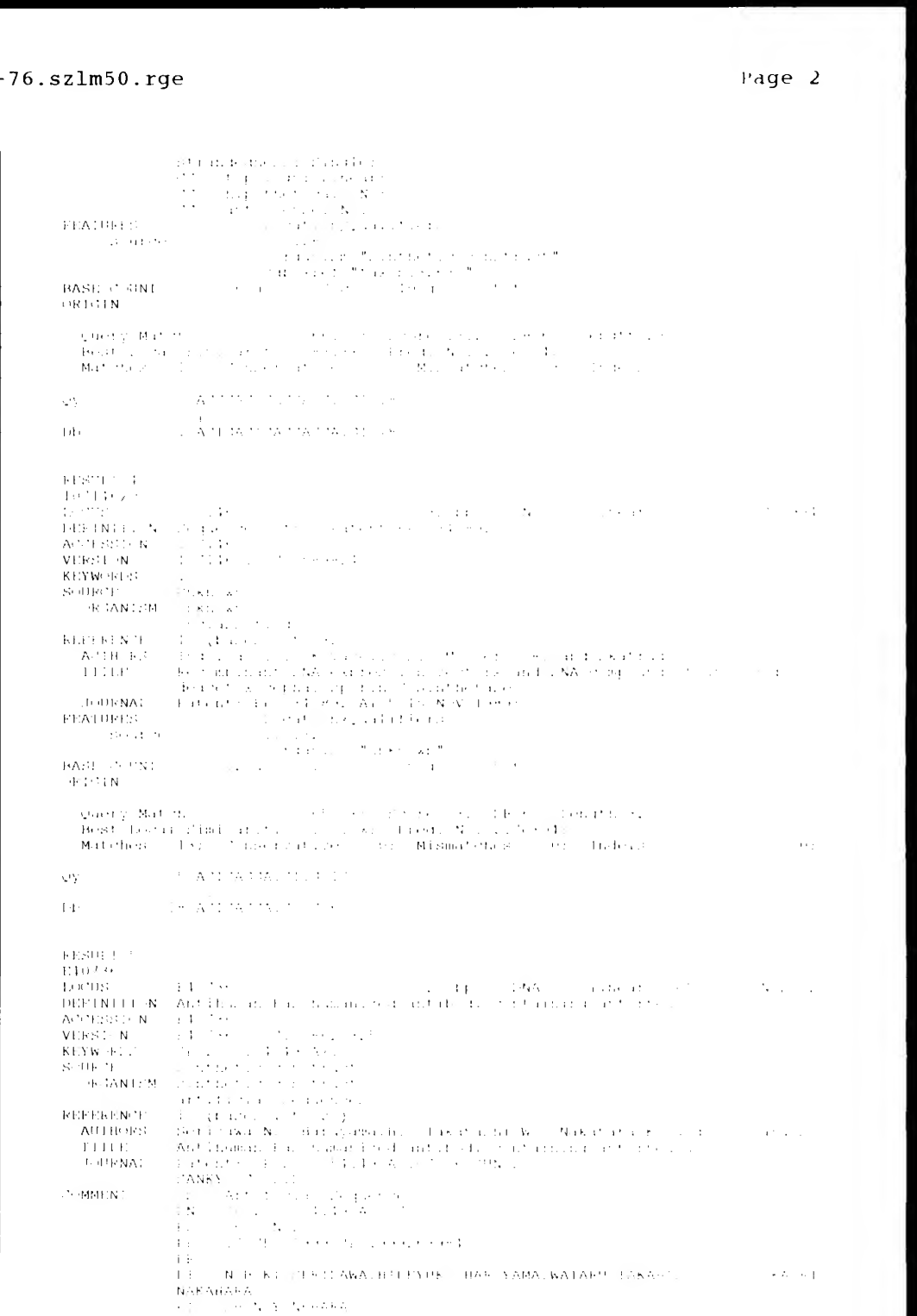
SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	[illegible]	[illegible]	[illegible]	[illegible]	AX[illegible]	[illegible]
2	[illegible]	[illegible]	31	6	AX[illegible]	[illegible]
3	13.2	66.0	28	6	E[illegible]	[illegible]
c 4	13	65.0	32	6	I07146	[illegible]
5	12.8	64.0	[illegible]	6	E[illegible]	[illegible]
6	12.8	64.0	24	6	E[illegible]	[illegible]
c 7	12.8	64.0	[illegible]	6	[illegible]	[illegible]
8	12.8	64.0	[illegible]	6	E[illegible]	[illegible]
c 9	12.8	64.0	30	6	AR064721	[illegible]
c 10	12.8	64.0	[illegible]	6	AR089[illegible]	[illegible]
11	12.8	64.0	[illegible]	6	AR1[illegible]	[illegible]
c 12	12.8	64.0	[illegible]	6	AX[illegible]	[illegible]
13	12.4	62.0	[illegible]	6	AR[illegible]	[illegible]
c 14	12.4	62.0	21	6	AR04[illegible]	[illegible]
15	12.4	62.0	21	6	AX0[illegible]	[illegible]
c 16	12.4	62.0	[illegible]	6	E[illegible]	[illegible]
c 17	12.4	62.0	[illegible]	6	E[illegible]	[illegible]
c 18	12.2	61.0	[illegible]	6	AX2[illegible]	[illegible]
c 19	12.2	61.0	28	6	BD[illegible]	[illegible]
20	12.2	61.0	31	6	AR090075	[illegible]
21	12.2	61.0	31	6	AR197[illegible]	[illegible]
22	12.2	61.0	[illegible]	6	AX201[illegible]	[illegible]
23	12.2	61.0	[illegible]	6	AX2[illegible]	[illegible]
c 24	12.2	61.0	34	6	AR14[illegible]	[illegible]
c 25	12.2	61.0	34	6	I27173	[illegible]
c 26	12.2	61.0	34	6	I32754	[illegible]
c 27	12.2	61.0	34	6	I84[illegible]	[illegible]
c 28	12.2	61.0	[illegible]	6	AX0[illegible]	[illegible]
29	12.2	61.0	[illegible]	6	AR14[illegible]	[illegible]
30	12.2	61.0	[illegible]	6	I27174	[illegible]
31	12.2	61.0	[illegible]	6	I32755	[illegible]
32	12.2	61.0	[illegible]	6	I84[illegible]	[illegible]
33	12.2	61.0	[illegible]	6	AX[illegible]	[illegible]
c 34	12	[illegible]	[illegible]	6	AR[illegible]	[illegible]
c 35	12	[illegible]	[illegible]	6	AR[illegible]	[illegible]
c 36	12	60.0	22	6	I85132	[illegible]
37	12	[illegible]	[illegible]	6	AR[illegible]	[illegible]
38	12	[illegible]	[illegible]	6	AX[illegible]	[illegible]
c 39	12	[illegible]	[illegible]	6	AX[illegible]	[illegible]
c 40	12	[illegible]	28	[illegible]	HUML[illegible]MP	[illegible]
c 41	12	60.0	28	[illegible]	HUML[illegible]MP	[illegible]
42	12	60.0	[illegible]	6	A[illegible]	[illegible]
43	12	[illegible]	[illegible]	[illegible]	AX[illegible]	[illegible]
c 44	12	[illegible]	[illegible]	[illegible]	AX[illegible]	[illegible]
c 45	12	[illegible]	[illegible]	[illegible]	AX[illegible]	[illegible]

ALIGNMENTS

RESULT 1
AX07665[illegible]
LOCUS AX[illegible] DNA linear [illegible]
DEFINITION Sequence [illegible] from Patent WO[illegible]
ACCESSION AX[illegible]
VERSION AX[illegible]
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to [illegible])
AUTHORS Boyle,W.[illegible] [illegible]
TITLE Combination therapy for conditions leading to bone [illegible]
JOURNAL Patent: WO [illegible]
Amgen [illegible]





SeqSearch version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Smith-Waterman search, using sw model

Run on: July 17, 2003, 18:52:32 ; Search time 144 Seconds
(without alignments)
312.778 Million cell updates/sec

Title: US-10-006-430-76

Perfect score: 20

Sequence: 1 acgaatcgcgaatcgtcgca 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searching: 2106240 seqs, 1125990150 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: N_Geneseq_120103:*
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25: /cgn2_6/ptodata/1/ngene/N_Geneseq_120103_dna.pep:*

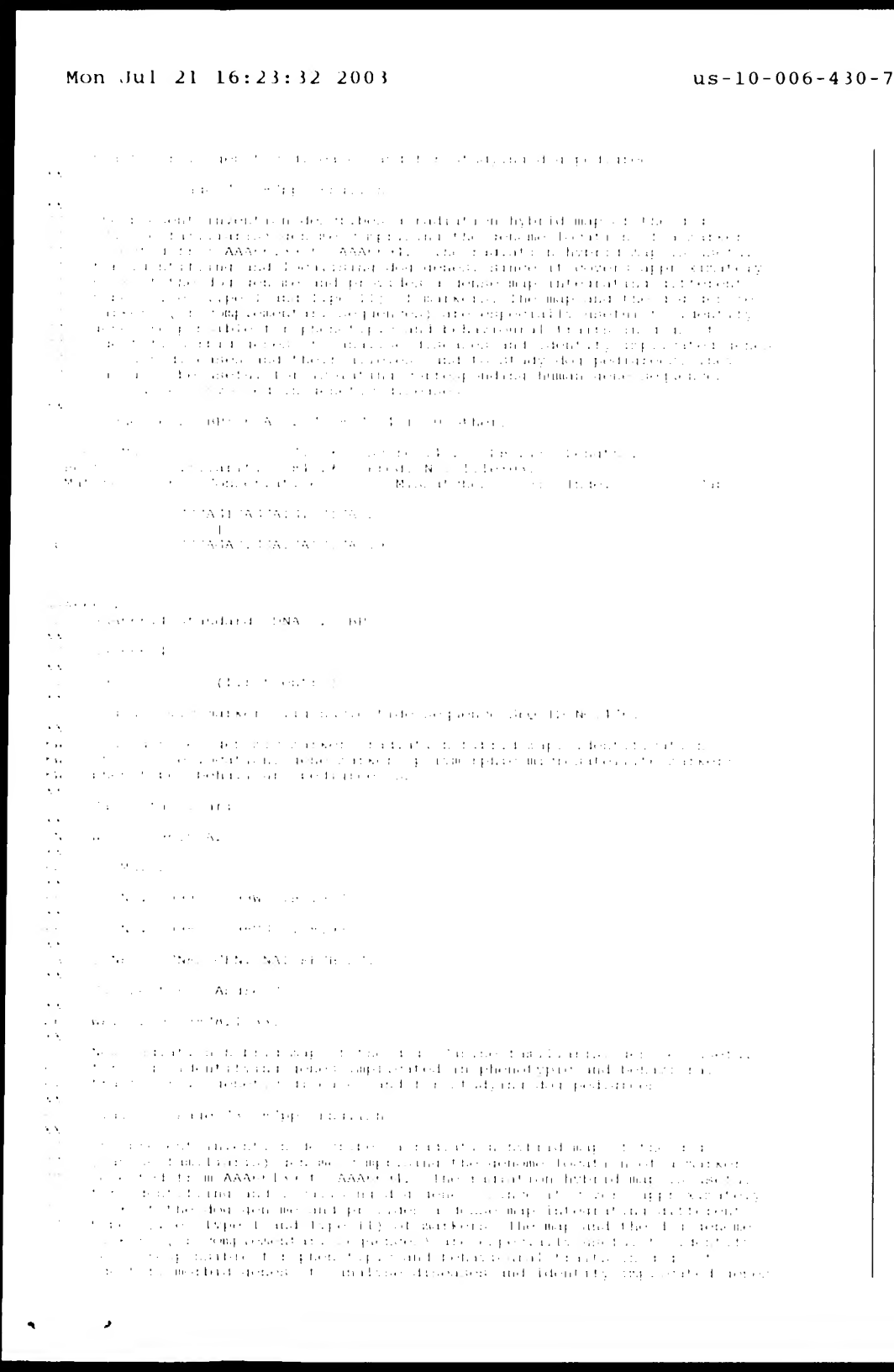
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, estimated by analysis of the total score distribution.

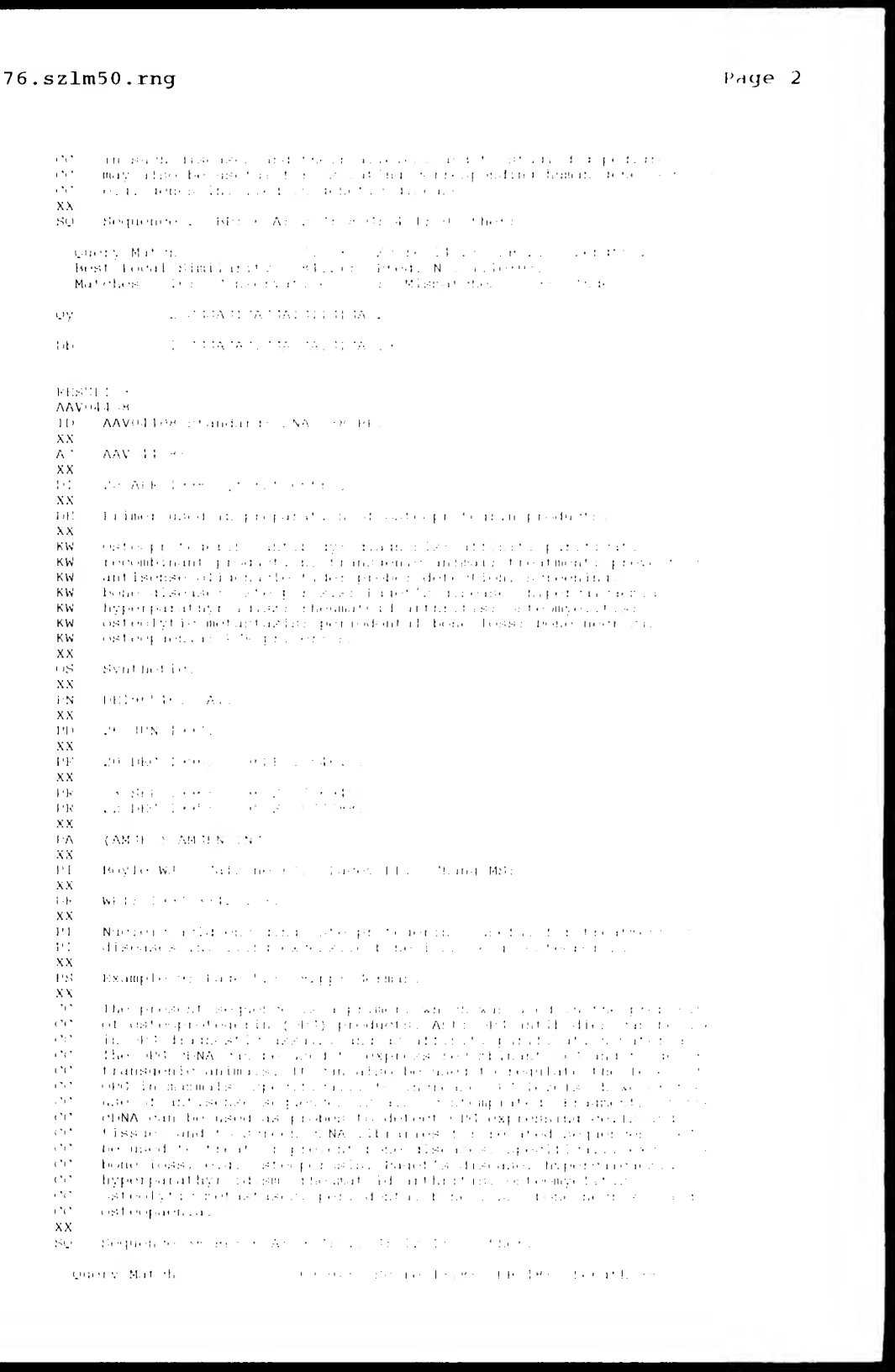
SUMMARIES

	Result No.	Score	Query Match	Length	DB ID	Description
	1	21.0	105	21	AAA66542	Dog genomic marker
	2	21.0	105	21	AAA66611	Dog genomic marker
	3	19.8	99	19	AAV94408	Primer used in pro
	4	19.0	95	22	AAE52808	Murine OPG mutagen
	5	18.8	94	22	AAI40952	Human single nucle
	6	18.8	94	20	AAI08244	p204, PCR primer 1
	7	18.8	94	20	AAI93499	Primer 2 for canin
	8	18.8	94	20	AAX17855	Primer #2 for cani
	9	18.8	94	21	AAA78408	Human Ig L chain s
	10	12.8	64.0	24	19	AAV88090	DNA sequence for
c	11	12.8	64.0	27	13	AAQ26429	Human DNA sequence
c	12	12.8	64.0	27	21	AAA38967	Human genomic seq
	13	12.8	64.0	29	20	AAX86771	PCR primer for
c	14	12.8	64.0	30	18	AAI72887	Primer #1 for ampl
	15	12.8	64.0	30	21	AAA87029	Mutant Ig light c
c	16	12.8	64.0	33	21	AAZ98202	Pt. 21 gene cDNA f
	17	12.8	64.0	36	16	AAQ84796	Spinach protein ki
c	18	12.8	64.0	50	24	ABA95147	Pt. 21 gene cDNA f
c	19	12.6	63.0	38	21	AAA59840	PCR primer for ge
	20	12.6	63.0	47	21	AAZ65821	Human 21q22.3 gene
c	21	12.4	62.0	20	20	AAX96374	PCR primer for
c	22	12.4	62.0	21	18	AA189554	Rice genomic DNA
c	23	12.4	62.0	23	20	AAZ33178	Rhodobacter DNA
	24	12.4	62.0	26	24	ABN99887	Human gene associa
	25	12.4	62.0	36	15	AAQ68732	Lambda-like polype
c	26	12.4	62.0	40	24	AAD26361	Mouse DNA sequence
c	27	12.2	61.0	18	21	AAZ73272	Human DNA sequence
	28	12.2	61.0	20	20	AAZ05795	PCR primer for
c	29	12.2	61.0	20	21	AAZ46646	Rotavirus VP2 gene
c	30	12.2	61.0	20	24	AB870771	Human gene DNA seq
c	31	12.2	61.0	21	20	AAZ38101	Human DNA sequence
c	32	12.2	61.0	21	20	AAZ31683	Human DNA sequence
	33	12.2	61.0	24	24	AB849469	Human DNA sequence
	34	12.2	61.0	25	22	AAS00228	AFX primer SEQ ID
c	35	12.2	61.0	26	24	AB846421	Probe 2 for detec
c	36	12.2	61.0	28	19	AAV22663	PCR primer for
	37	12.2	61.0	31	24	AB866107	Human DNA sequence
	38	12.2	61.0	33	22	AAS64141	Human gene associa
	39	12.2	61.0	33	22	AAP03996	Human gene associa
	40	12.2	61.0	35	24	AB195602	Human DNA sequence
c	41	12.2	61.0	35	20	AAP59668	HBV polymerase DNA
	42	12.2	61.0	37	21	AB092509	Pt. 21 gene cDNA f
	43	12.2	61.0	41	21	AAA39512	EBV nuclear antig
	44	12.2	61.0	45	16	AAX11139	Human DNA sequence
c	45	12	60.0	29	20	AAY99363	Human DNA sequence

ALIGNMENTS

RESULT 1
AAA66542
ID AAA66542 standard; DNA; 20 BP.
XX
AC AAA66542;
XX
DT 09-OCT-2000 (first entry)
XX
DE Dog genomic marker oligonucleotide sequence SEQ ID NO 94.
XX
KW Dog; genome; genomic marker; radiation hybrid map; identity;
KW chromosome location; gene marker; polymorphic microsatellite;
KW phenotype; behaviour; pedigree; ss.
XX
OS Canis familiaris.
XX
PN WO200029615-A2.
XX
PD 25-MAY-2000.
XX
PF 15-NOV-1999; 99WO-IB01997.
XX
PR 13-NOV-1998; 98US-0108193.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Galibert F, Andre C;
XX
DR WPI; 2000-387821/33.
XX
PT New radiation hybrid map of the dog, Canine familiaris, specific
PT for e.g. identifying genes implicated in phenotype and beha





Qy 4 GAGTCAGGATGTTGTGCA 20
||||||||||||| | |
Db 9 GAGTCAGGATGTTTTCCA 25

RESULT 5
AAI30957/c
ID AAI30957 standard; DNA; 31 BP.
XX
AC AAI30957;
XX
DT 18-OCT-2001 (first entry)
XX
DE Human single nucleotide polymorphism (SNP) HIVEP1 5.
XX
KW Human; resequence; genotype; disease; forensic; paternity [illegible]
KW single nucleotide polymorphism; SNP; ss.
XX
OS Homo sapiens.
XX
FH Key Location/qualifiers
FT Variation replace(16,1)
FT /*tag= a
FT /standard_name= "single nucleotide polymorph[illegible]"
XX
PN WO200166800-A2.
XX
PD 13-SEP-2001.
XX
PF 07-MAR-2001; 2001WO-US07268.
XX
PR 07-MAR-2000; 2000US-0187510.
PR 22-MAY-2000; 2000US-0206129.
XX
PA (WHEH-) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Cargill M, Ireland JS, Lander ES;
XX
DR WPI; 2001-522952/57.
XX
PT Nucleic acid molecules from the human genome which include p[illegible]
PT sites, useful in methods for predicting the presence, absence
PT severity of a particular phenotype or disorder (e.g. diabetes
PT associated with a particular genotype
XX
PS Claim 1; Page 119; 145pp; English.
XX
CC The invention relates to the identification of nucleic acid[illegible]
CC (AAI29513 AAI31814) from the human genome which include polym[illegible]
CC which can predispose individuals to disease. Various genes [illegible]
CC of individuals were resequenced and single nucleotide polymorp[illegible]
CC (SNPs) in these genes discovered. The method is useful for pr[illegible]
CC presence, absence or severity of a particular phenotype or dis[illegible]
CC diabetes) associated with a particular genotype. The nucleic a[illegible]
CC containing the polymorphic sites may be useful in forensics a[illegible]
CC testing.
XX
SQ Sequence 31 BP; 5 A; 12 C; 6 G; 8 T; 0 other;

Query Match 67.0%; Score 13.4; DB 22; Length 31;
Best Local Similarity 93.3%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CTCAGGATGTTGTGA 20
||||||||||| |||
Db 31 CTCAGGATGTTGTGA 17

RESULT 6
AAT08244/c
ID AAT08244 standard; DNA; 20 BP.
XX

[illegible] Claim 7; 27pp; English.
XX
[illegible] AAX17821-X17860 are used to PCR amplify microsatellite repeat sequences from loci of canine genotypes. The primers AAX17835 and AAX17[illegible] are used to amplify the locus 15 repeat sequence. The repeat sequences can be used in a method for genotyping a canine, by PCR amplifying a region of chromosomal DNA with primers that specifically hybridise to a microsatellite locus, where the region comprises: (a) a repeated tetranucleotide motif consisting of AAA or TTT and a fourth nucleotide; or (b) a repeated motif selected from AAAG, GAAA, AAAT, TTTC, [illegible], TTTA, AAGG, GAAT, GAAG, GAAAA, AAAAAG, TGC and TTC. The amplification product is size fractionated to provide a measure of the size of the chromosomal DNA between the primers, where the size of the amplification product is polymorphic for the locus and provides a genotype for the canine. The combined information from multiple loci provides a means of distinguishing individuals, even among inbred dog breeds, for parentage testing, forensic testing and analysis of [illegible] relatedness.
XX
SQ Sequence [illegible] BP; 4 A; [illegible] C; 5 G; 8 T; 0 other;

Query Match 64.0%; Score 12.8; DB 20; Length 20;
Best Local Similarity 87.5%; Pred. No. 5.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GA[illegible]CAGGATGTTGTG 18
[illegible]
Db 1 GAGCAGGATGTTGTG 16

RESULT 9
AAA7[illegible]
ID AAA7[illegible] standard; DNA; 20 BP.
XX
AC AAA7[illegible];
XX
DT [illegible] (first entry)
XX
DE [illegible] chain sequencing primer SHKF 4.
XX
KW Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer; immunosuppression; autoimmune disease; treatment; rheumatism; [illegible] antibody; primer; ss.
XX
OS [illegible]
XX
PN [illegible] 114 A.
XX
PD [illegible]
XX
PF [illegible] 98JP 026[illegible]04.
XX
PR [illegible] 98JP 0264508.
XX
PA (SANK) SANKYO CO LTD.
XX
DR WPI; [illegible] 154476/40.
XX
PT Anti human Fas humanizing antibody containing antirheumatic agents
XX
PS [illegible] 1; Page 21; [illegible]pp; Japanese.
XX
CC The present invention relates to antirheumatic agents which comprise as [illegible] ingredients an immunoglobulin M (IgM) protein. The IgM protein [illegible] include a J segment, has apoptosis inducing activity, and [illegible] of a light and heavy chain polypeptide produced synthetically. The agents of the invention exhibit antirheumatic and immunosuppressive activity and can be used to treat autoimmune diseases, especially rheumatism. The IgM molecule used in the invention has human Fas antigen [illegible] properties. Included in the invention are nucleotide sequences [illegible] the IgM light and heavy chains (see AAA78267-A78272) and the [illegible] protein sequences (see AAB12913-B12918 and AAB12919), and [illegible] sequences of the humanised anti human Fas Ig CHII (see
CC AAA78202-A78206) and protein sequences (see AAB12908-B12912). [illegible] included are anti-human Fas antibody CDR peptides (AAB12902-[illegible]). Primers specific for the anti-human Fas antibody, light, heavy and [illegible] chains used in the invention are represented by sequences AAA78213-A78266. Primers used for sequencing the human Ig DNA [illegible] invention are represented by sequences AAA78277-A78318 and AAA78335-A78337, while humanised anti Fas Ig DNA sequencing [illegible] represented by sequences AAA78321-A78334 and AAA78338-A78[illegible]. [illegible] sequences AAA78207-A78212 are specific for murine Ig DNA, and [illegible] the production of the agent of the invention.
XX
SQ Sequence 20 BP; 3 A; 2 C; 8 G; 7 T; 0 other;

Query Match 64.0%; Score 12.8; DB 21; Length 20;
Best Local Similarity 87.5%; Pred. No. 5.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels [illegible]

Qy 5 AGTCAGGATGTTGTGA 20
||| ||||||||||||
Db 4 AGTGGGGATGTTGTGA 19

RESULT 10
AAV30090
ID AAV30090 standard; DNA; 24 BP.
XX
AC AAV30090;
XX
DT 12-AUG-1998 (first entry)
XX
DE DNA sequence used to screen a cancer metastasis inhibiting [illegible]
XX
KW Screening; inhibition; cancer metastasis; Ets 1 protein; ss.
XX
OS Unidentified.
XX
PN JP10137000-A.
XX
PD 26-MAY-1998.
XX
PF 01-NOV-1996; 96JP-0305486.
XX
PR 01-NOV-1996; 96JP-0305486.
XX
PA (SUNR) SUNTORY LTD.
PA (TANI/) TANIGUCHI N.
XX
DR WPI; 1998-355054/31.
XX
PT Screening for inhibitors of cancer metastasis - comprises [illegible]
PT DNA with Ets 1 protein or its fragment and sample, and measuring [illegible]
PT extent of complexing
XX
PS Claim 1; Page 2; 11pp; Japanese.
XX
CC The present sequence is used in the method of the invention. [illegible]
CC specification describes a new method for screening a compound [illegible]
CC inhibiting metastasis of cancer. The method comprises incubat[illegible]
CC containing the present sequence with an Ets 1 protein or its [illegible]
CC and a sample, and measuring the amount of DNA/Ets 1 protein [illegible]
CC that form. The method is useful for the primary screening [illegible]
CC metastasis inhibiting substance.
XX
SQ Sequence 24 BP; 7 A; 0 C; 13 G; 4 T; 0 other;

Query Match 64.0%; Score 12.8; DB 19; Length 24;
Best Local Similarity 87.5%; Pred. No. 5.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels [illegible]

Qy 3 GGAGTCAGGATGTTGT 18
||||| |||||| |||
Db 2 GGAGTGAGGATGAGGT 17

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XX
[illegible]
XX
[illegible] (first entry)
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[illegible]
XX
[illegible] oxygen exchange [illegible] HIV [illegible]
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[illegible]
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[illegible] ALABAMA [illegible]
XX
[illegible]
XX
[illegible] AAB[illegible]
XX
[illegible] human haemoglobin [illegible]
[illegible] free blood substitute
XX
[illegible]
XX
[illegible] primer which was used [illegible]
[illegible] and third [illegible] in the human beta globin [illegible] The
[illegible] molecule encoded by this mutated gene has oxygen exchange
[illegible] close to natural haemoglobin (Hb)
[illegible] use in a cell free blood substitute. The mutated gene
[illegible] for expression of [illegible] modified human
[illegible] of non human transgenic animals. The Hb [illegible]
[illegible] can be used without the need for blood [illegible]
[illegible] transgenic Hb will be free [illegible] viruses as HIV
XX
[illegible]

[illegible] Match [illegible] Score [illegible] DB [illegible] Length [illegible]
[illegible] Similarity [illegible] Pred. No. [illegible]
[illegible] Conservative [illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]

[illegible]
[illegible]
[illegible]


[illegible]
[illegible]
[illegible] standard; DNA; [illegible]
XX
[illegible]
XX
[illegible] (first entry)
XX
[illegible] protein [illegible] receptor [illegible] PCR primer [illegible]
XX
[illegible] receptor [illegible]
[illegible] response [illegible]
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200[illegible] A1.
XX
PD 20 APR [illegible]
XX
PF 08 OCT [illegible] [illegible]
XX
PR 09 OCT 1998; [illegible]
PR 07 DEC 1998; [illegible]
PR 21 DEC 1998; [illegible]
XX
PA (CHUG ) [illegible] MOLECULAR MEDICINE [illegible]
XX
PI Maeda M, Nakata [illegible]
XX
DR WPI; 200[illegible]
XX
PT Novel G protein coupled receptor proteins encoded by the [illegible]
PT receptor gene family, are useful in screening drugs [illegible]
PT regulate the control of the immune response and hematop[illegible]
XX
PS Example [illegible] Page [illegible] Japanese.
XX
CC The present sequence represents a PCR primer for a G p[illegible]
CC receptor protein, isolated from human, which is [illegible]
CC immune response and control of haematopoiesis. The [illegible]
CC receptors from the present invention have immunomodulatory [illegible]
CC haematopoiesis regulatory activities. The G protein coupled [illegible]
CC and nucleotide sequences encoding them can be used in [illegible]
CC or their ligands [illegible] regulate the functions of immune [illegible]
CC haematopoiesis control.
XX
SQ Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

Query Match [illegible] Score [illegible] DB [illegible] Length [illegible]
Best Local Similarity [illegible] Pred. No. [illegible]
Matches 14; Conservative [illegible] Mismatches [illegible] Indels [illegible]

Qy [illegible]
[illegible]
Db [illegible]


RESULT 1[illegible]
AAX86[illegible]
ID AAX86[illegible] standard; DNA; [illegible] BP.
XX
AC AAX86[illegible]
XX
DT 20 SEP 199[illegible] (first entry)
XX
DE PCR primer [illegible]
XX
KW Genetic mutant [illegible]
KW PCR primer; ss.
XX
OS Synthetic.
XX
PN JP11[illegible] A
XX
PD 29 JUN 199[illegible]
XX
PF 10 DEC 199[illegible] [illegible]
XX
PR 10 DEC 199[illegible] [illegible]
XX
PA (MIHI ) MITSUBISHI [illegible]
XX
DR WPI; 199[illegible]
XX
```

```
PT   [illegible] system for secretion of protein in a medium - uses a specific
PT   [illegible] protein from Corynebacterium
XX
PS   [illegible] Page 7; 10pp; Japanese.
XX
CC   [illegible] invention describes a new genetic mutant system that comprises a
CC   protein having a sequence shown in AAY2[illegible], in which the amino acid
CC   residue 44 is Phe. A Corynebacterium cell can be transformed with a
CC   recombinant plasmid containing the DNA encoding the mutant protein. The
CC   [illegible] is used to secrete a target protein in a medium. A system
CC   [illegible] efficiently a specified protein in a medium can be
CC   constructed. The system using the protein having mutant sequence secrets
CC   a specified protein in a Corynebacterium more efficiently than a
CC   secretion system constituted by including a protein having a sequence
CC   shown in AAY27002 where amino acid residue 44 is Val. Sequences
CC   AAX[illegible] represent PCR primers used during the course of the
CC   invention.
XX
SQ   Sequence [illegible] BP; [illegible] A; 7 C; 7 G; 9 T; 0 other;

  Query Match             64.0%;  Score 12.8;  DB 20;  Length 29;
  Best Local Similarity   87.5%;  Pred. No. [illegible];
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

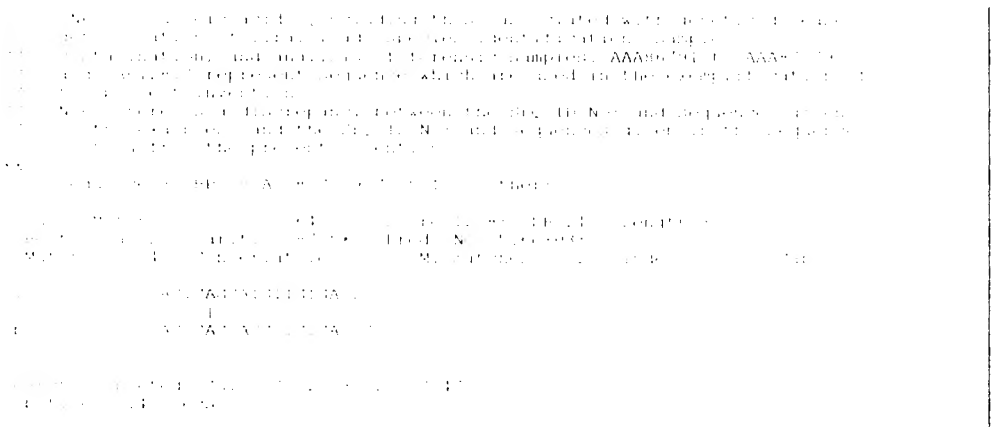
Qy          [illegible] ACTGAGTCAGGATCTT 16
              ||||||||| || ||
Db          [illegible] ACGGATCAGAATCTT 29


RESULT [illegible]
AA[illegible]
ID   AA[illegible] standard; DNA; 30 BP.
XX
AC   A[illegible];
XX
DT   [illegible] (first entry)
XX
DE   [illegible] #1 for cysteine rich region of DABP.
XX
KW   [illegible] amplify; polymerase chain reaction; DBL gene family; SABP;
KW   [illegible] acid binding protein; Duffy antigen binding protein; erythrocyte;
KW   [illegible] merozoite; malaria; var 1; var 2; var 3; var 7; vaccine; therapy;
KW   [illegible] response; Plasmodium; ss.
XX
OS   [illegible]
XX
PN   W[illegible] A1.
XX
PD   [illegible]
XX
PF   [illegible] 98WO-US[illegible].
XX
PR   [illegible] 95US [illegible].
XX
PA   [illegible] US DEPT HEALTH & HUMAN SERVICES.
XX
PI   [illegible] Miller LH, Peterson DS, [illegible] KL, Su X;
PI   W[illegible] JD;
XX
DR   WPI; [illegible]/0[illegible].
XX
PT   [illegible] containing cysteine rich DBL family protein
PT   [illegible] domains homologous domains of the Duffy and sialic acid
PT   [illegible] proteins
XX
PS   [illegible] 21; [illegible]pp; English.
XX
CC   [illegible] and AAI72887 represent amplification primers for the cysteine
CC   [illegible] region of the coding sequence (see AAI72889 for full length coding
CC   [illegible]) for the Duffy antigen binding protein (DABP). DABP and the
CC   [illegible] acid binding protein (SABP) are soluble proteins that appear in
CC   the [illegible] supernatant after infected erythrocytes release merozoites.
CC   DABP and SABP mediate the binding of merozoites and schizonts to the
CC   erythrocyte surface. These proteins are necessary for eryth[illegible]
CC   invasion by the parasite. The amplified sequence can be used [illegible]
CC   compositions of the invention. The compositions are for the [illegible]
CC   and prevention of malaria, and comprise either a nucleotide [illegible]
CC   encoded polypeptide of the var 1, var-2, var-3 or var 7 gene[illegible]
CC   gene family, a family of genes having homology with conser[illegible]
CC   DABP and SABP. The compositions are used for the treatment a[illegible]
CC   prevention of malaria. They are also used in the preparation [illegible]
CC   for inducing a protective immune response in a mammal to Plas[illegible]
CC   merozoites (especially Plasmodium falciparum or Plasmodium [illegible])
XX
SQ   Sequence 30 BP; 6 A; 9 C; 8 G; 7 T; 0 other;

  Query Match             64.0%;  Score 12.8;  DB 18;  Length 3[illegible];
  Best Local Similarity   87.5%;  Pred. No. [illegible];
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    [illegible]

Qy          5 ACTCAGGATGTTGTGA 20
              | ||||| |||||||
Db         30 ACTCAGGAAGTTGTGA 15


RESULT 15
AAA87029
ID   AAA87029 standard; DNA; 30 BP.
XX
AC   AAA87029;
XX
DT   15-JAN-2001  (first entry)
XX
DE   Mutant target oligonucleotide.
XX
KW   Detection; nucleic acid hybrid; depolymerisation; analysis; [illegible]
KW   single nucleotide polymorphism; identification; viral load; [illegible]
KW   genotyping; medical marker diagnostic; primer; target; mutat[illegible]
KW   genetic disease; ss.
XX
OS   Synthetic.
XX
PN   WO200049180-A1.
XX
PD   24-AUG-2000.
XX
PF   18-FEB-2000; 2000WO-US04242.
XX
PR   18-FEB-1999;   99US-0252436.
PR   21-JUL-1999;   99US-0358972.
PR   25-AUG-1999;   99US-0383316.
XX
PA   (PROM-) PROMEGA CORP.
XX
PI   Shultz JW,  Lewis MK,  Leippe D,  Mandrekar M,  Kephart D,  [illegible]
PI   Andrews CA,  Hartnett JR,  Gu T,  Olson KJ,  Wood KV,  Welch [illegible]
XX
DR   WPI; 2000-565377/52.
XX
PT   Determining presence or absence of a predetermined endogenous [illegible]
PT   acid sequence by using an enzyme that depolymerizes the 3' end [illegible]
PT   oligonucleotide probe hybridized to a target sequence to rele[illegible]
PT   identifier nucleotides
XX
PS   Example; Page 360; 389pp; English.
XX
CC   The present invention describes a method (M1) for determinin[illegible]
CC   presence or absence of a predetermined endogenous nucleic ac[illegible]
CC   sequence (ENAT). The method comprises hybridising a probe fo[illegible]
CC   identifier nucleotide (IN) with ENAT which is treated with a[illegible]
CC   that depolymerises the 3' end of hybridised NA to release th[illegible]
CC   M1 is used for determining the number of known sequence repe[illegible]
CC   in a nucleic acid target sequence in a nucleic acid sample. [illegible]
CC   is also useful for determining whether a nucleic acid target [illegible]
CC   a sample is an allele from a homozygous or heterozygous locu[illegible]
CC   method is also useful for detection of mutations, transloca[illegible]
```



[illegible] search, using sw model

Run on: July 17, 2003, [illegible]; Search time 1106 Seconds
(without alignments)
2[illegible].866 Million cell updates/sec

Title: US-10-006-430-76
[illegible]
Sequence: 1 [illegible] 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_est[illegible]:*
6: em_estpl:*
7: em_est[illegible]:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

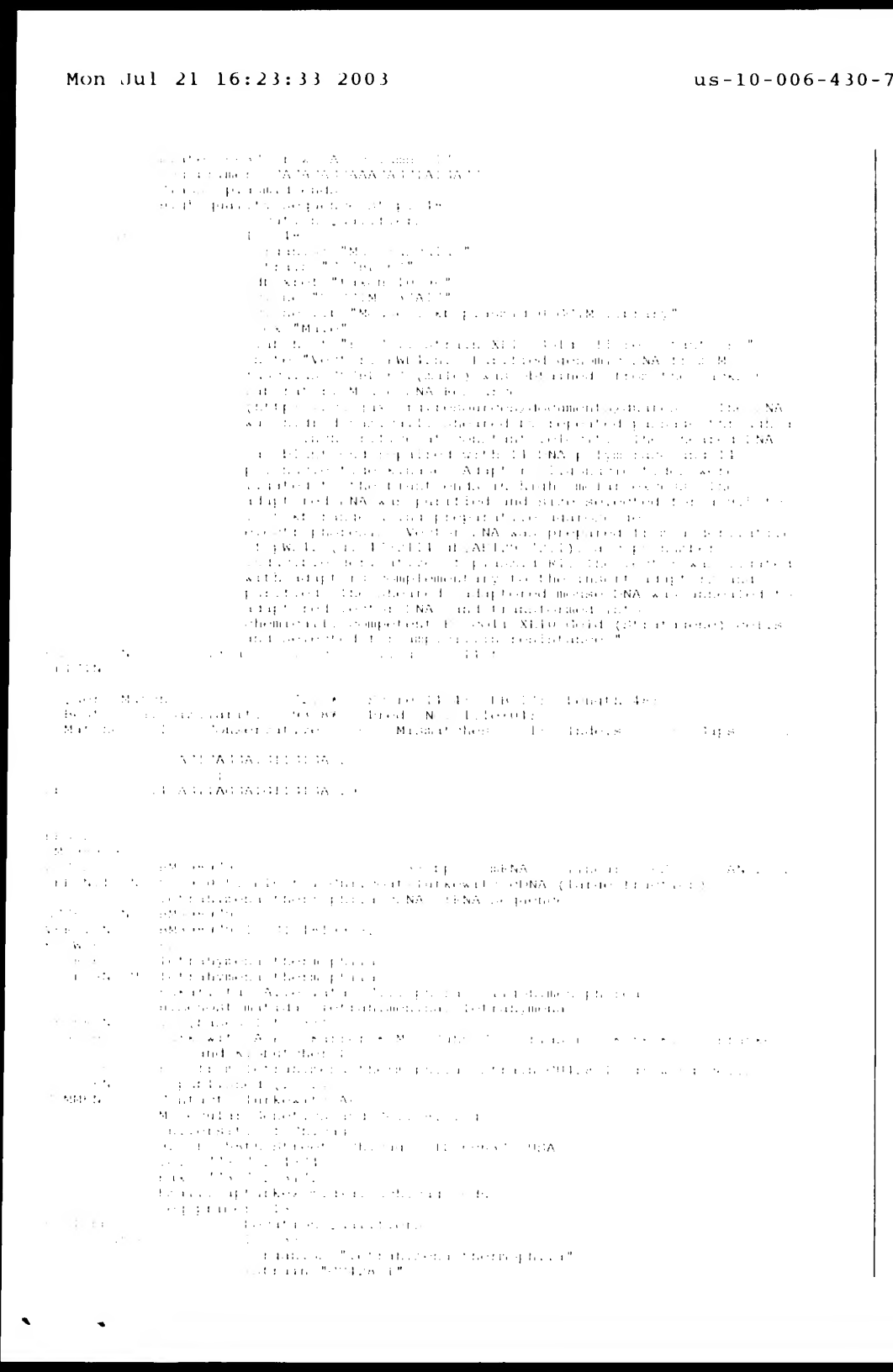
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	[illegible]	[illegible]	49	17	AZ[illegible]	AZ[illegible] [illegible]
2	[illegible]	[illegible]	[illegible]	[illegible]	BM[illegible]	BM[illegible] [illegible]
3	[illegible]	[illegible]	45	17	BH[illegible]	BH[illegible] [illegible]
4	[illegible]	[illegible]	[illegible]	[illegible]	AI[illegible]	AI[illegible] [illegible]
5	[illegible]	63.0	50	[illegible]	AU[illegible]	AU[illegible] AU[illegible]
6	[illegible]	[illegible]	[illegible]	[illegible]	AZ[illegible]	AZ[illegible] [illegible]
c 7	12.2	[illegible]	[illegible]	17	AZ[illegible]	[illegible]
c 8	12.2	61.0	50	9	AU102676	[illegible]
c 9	12	[illegible]	[illegible]	17	AZ[illegible]	[illegible]
c 10	12	[illegible]	43	17	AZ807[illegible]	[illegible]
11	12	60.0	50	9	AU[illegible]	[illegible]
12	12	[illegible]	50	9	AU[illegible]	[illegible]
c 13	11.8	59.0	41	17	[illegible]	[illegible]
14	11.8	[illegible]	43	13	[illegible]	[illegible]
c 15	11.6	58.0	40	9	AI080507	[illegible]
16	11.6	58.0	40	17	[illegible]	[illegible]
c 17	11.6	58.0	42	13	[illegible]	[illegible]
c 18	11.6	58.0	43	9	AA[illegible]	[illegible]
c 19	11.6	[illegible]	47	17	AZ[illegible]	[illegible]
c 20	11.6	58.0	47	17	AZ767804	[illegible]
21	11.6	[illegible]	49	14	[illegible]	[illegible]
c 22	11.4	57.0	37	9	AU256480	[illegible]
23	11.2	56.0	41	17	AZ[illegible]	[illegible]
24	11.2	[illegible]	42	9	AI8[illegible]	[illegible]
25	11.2	56.0	43	9	AA972845	[illegible]
26	11.2	[illegible]	43	17	AZ[illegible]	[illegible]
27	11.2	56.0	45	17	AZ480635	[illegible]
28	11.2	[illegible]	48	17	AL[illegible]	[illegible]
c 29	11.2	[illegible]	50	9	AU[illegible]	[illegible]
30	11.2	56.0	50	9	AU103858	[illegible]
c 31	11.2	[illegible]	50	9	AU[illegible]	[illegible]
32	11	55.0	32	13	BI818900	[illegible]
33	11	[illegible]	32	13	BI[illegible]	[illegible]
c 34	11	55.0	35	14	[illegible]	[illegible]
c 35	11	55.0	37	14	[illegible]	[illegible]
36	11	[illegible]	43	9	AA[illegible]	[illegible]
37	11	55.0	44	17	AZ787[illegible]	[illegible]
38	11	[illegible]	45	13	[illegible]	[illegible]
c 39	11	55.0	46	14	[illegible]	[illegible]
40	11	[illegible]	48	17	BH[illegible]	[illegible]
41	11	[illegible]	50	9	AU[illegible]	[illegible]
42	11	55.0	50	9	AU[illegible]	[illegible]
43	10.8	[illegible]	25	17	AZ[illegible]	[illegible]
c 44	10.8	54.0	26	17	AZ44[illegible]784	[illegible]
c 45	10.8	[illegible]	27	17	BH[illegible]	[illegible]

ALIGNMENTS

RESULT 1
AZ318461
LOCUS AZ318461 [illegible] bp DNA linear [illegible]
DEFINITION [illegible] Mouse [illegible] plasmid [illegible] library [illegible] clone [illegible] DNA sequence.
ACCESSION AZ318461
VERSION AZ318461.1 [illegible]
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; [illegible]
REFERENCE 1 (bases 1 to 48)
AUTHORS [illegible], Aoyagi,A., Barber,M., [illegible] Islam,R., [illegible], Mahmoud,M., [illegible] M., Rose,M., Rose,R., Stokes,R., [illegible] and Wright,T., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads [illegible] plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
[illegible] Biomedical Polymers Research Bldg., [illegible]
[illegible], USA
Tel: 801 [illegible]
Fax: 801 [illegible]
Email: [illegible]
Insert Length: [illegible] Std Error: [illegible]



```
Qy          1 ACGGAGTCAGGAGATGTTGTG 17
              ||||||| |||| |||
Db          3 ACGAGTCGGGATGTTG 18


RESULT 4
AI642028
LOCUS       AI642028                  40 bp    mRNA    linear   EST 29-APR-1999
DEFINITION  vb74b04.x1 Soares mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1383511 3' similar to SW:UCP3 MOUSE P56501 MITOCHONDRIAL
            UNCOUPLING PROTEIN 3 ;, mRNA sequence.
ACCESSION   AI642028
VERSION     AI642028.1  GI:4720503
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:905479
            This clone was previously sequenced on the 5' end only, this new
            data is from the 3' end
            Possible reversed clone: similarity on wrong strand
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1..40
                     /organism "Mus musculus"
                     /db_xref "taxon:10090"
                     /clone "IMAGE:1383511"
                     /clone_lib "Soares mammary gland NMLMG"
                     /sex "female (lactating)"
                     /tissue_type "mammary gland"
                     /lab_host "DH10B"
                     /note "Vector: pT7T3D Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector. Library is normalized. Library
                     was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT        5 a      18 c      7 g      10 t
ORIGIN

  Query Match             63.0%;  Score 12.6;  DB 9;  Length 40;
  Best Local Similarity   78.9%;  Pred. No. 6.4e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ACGGAGTCAGGAGATGTTGTG 19
              | |||||||||   ||||
Db         24 AACGAGTCAGGGGCTTGTG 6


RESULT 5
AU160832
LOCUS       AU160832                  50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU160832 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HRC10538, mRNA sequence.
ACCESSION   AU160832
VERSION     AU160832.1  GI:15533353
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J. ...
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K. ...
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine ...
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. ...
            ,S. Construction and characterization of a full length ...
            a 5'-end enriched cDNA library. Gene 200 (1-2), 149-...
FEATURES             Location/Qualifiers
     source          1..50
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "HRC10538"
                     /clone_lib "Sugano Homo sapiens cDNA library"
                     /note "Differential display comparison of ...
                     dimethylfumarate treated U937 cells"
BASE COUNT        6 a      12 c      16 g      16 t
ORIGIN

  Query Match             63.0%;  Score 12.6;  DB 9;  Length 50;
  Best Local Similarity   78.9%;  Pred. No. 7e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    ...

Qy          1 ACGGAGTCAGGATGTTGTG 19
              ||| |||||  | |||||
Db         32 ACGTAGTCAGGTCTTGTG 50


RESULT 6
AZ817361
LOCUS       AZ817361                  50 bp    DNA     linear   ...
DEFINITION  2M0086K21R Mouse 10kb plasmid UUGC2M library Mus musc...
            clone UUGC2M0086K21 R, DNA sequence.
ACCESSION   AZ817361
VERSION     AZ817361.1  GI:12987365
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E...
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; M...
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,L., Duval,B. ...
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pederse...
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niede...
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads ...
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2...
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0086  row: K  column: 21
            Seq primer: CACACAGGAAACAGCTATGAC
            Class: plasmid ends
            High quality sequence stop: 50.
FEATURES             Location/Qualifiers
     source          1..50
                     /organism "Mus musculus"
                     /strain "C57BL/6J"
```

ORIGIN

Query Match 61.0%; Score 12.2; DB 9; Length 50;
Best Local Similarity 82.4%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGAGTCAGGATGTTGTG 19
Db 18 GGAGTCAGCTGGTTGTG [illegible]

RESULT 9
AZ346681/c
LOCUS AZ346681 43 bp DNA linear GSS 29 SEP 2000
DEFINITION 1M0082G01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0082G01 F, DNA sequence.
ACCESSION AZ346681
VERSION AZ346681.1 GI:10425918
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 43)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,L., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: G column: 01
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 43.
FEATURES Location/Qualifiers
source 1..43
/organism "Mus musculus"
/strain "C57BL/6J"
/db_xref "taxon:10090"
/clone "UUGC1M0082G01"
/clone_lib "Mouse 10kb plasmid UUGC1M library"
/sex "Male"
/lab_host "E. coli strain XL10 Gold, Tl resistant, F-"
/note "Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource [illegible] was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XL10 Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 6 a 27 c [illegible] g [illegible] t

ORIGIN

Query Match 60.0%; Score 12; DB 17; Length 43;
Best Local Similarity 75.0%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 5; Indels [illegible]

Qy 1 ACGGAGTCAGGATGTTGTGA 20
Db 25 AAGGAGTGAGGAGGGGGTGA 6

RESULT 10
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DEFINITION 2M0069G09R Mouse 10kb plasmid UUGC2M library Mus musculus [illegible] clone UUGC2M0069G09 R, DNA sequence.
ACCESSION AZ807113
VERSION AZ807113.1 GI:12971138
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible] Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; [illegible]
REFERENCE 1 (bases 1 to 43)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,L., Duval,B., [illegible] Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,[illegible] ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Nieder[illegible] and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads [illegible] plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. [illegible] 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0069 row: G column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 43.
FEATURES Location/Qualifiers
source 1..43
/organism "Mus musculus"
/strain "C57BL/6J"
/db_xref "taxon:10090"
/clone "UUGC2M0069G09"
/clone_lib "Mouse 10kb plasmid UUGC1M library"
/sex "Male"
/lab_host "E. coli strain XL10 Gold, Tl resistant, F-"
/note "Vector: PWD42nv; Purified genomic DNA [illegible] musculus C57BL/6J (male) was obtained from [illegible] Laboratory Mouse DNA Resource [illegible] was hydrodynamically sheared by repeated passage [illegible] 0.005 inch orifice at constant velocity. The [illegible] was blunt end repaired with T4 DNA polymerase [illegible] polynucleotide kinase. Adaptor oligonucleotides [illegible] ligated to the blunt ends in high molar excess. [illegible] adaptored DNA was purified and size selected [illegible] 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared [illegible] of pWD42 (gi|4732114|gb|AF129072.1), a copy [illegible] inducible derivative of plasmid R1. The vector [illegible] with adaptors complementary to the insert adaptors [illegible] purified. The sheared, adaptored mouse DNA was [illegible] adaptored vector DNA, and transformed into chemically competent E. coli XL10 Gold (Stratagene) [illegible] and selected for ampicillin resistance."
BASE COUNT 14 a 10 c 7 g 12 t

[illegible]
LOCUS BI452697 43 bp mRNA linear EST 11 DEC 2001
DEFINITION BI452697 NIBB Mochii normalized Xenopus neurula library, Xenopus laevis cDNA clone XL042111 5', mRNA sequence.
ACCESSION BI452697
VERSION BI452697.1 GI:17198743
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 43)
AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara Y.
TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81 [illegible]
Fax: 81 [illegible]
Email: tshin [illegible].ac.jp.
FEATURES Location/Qualifiers
source 1..43
/organism "Xenopus laevis"
/db_xref "taxon:8355"
/clone "XL042111"
/clone_lib "NIBB Mochii normalized Xenopus neurula library"
/tissue_type "whole embryo"
/dev_stage "stage 15"
/note "Vector: pBSSN; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn (Wellcome/CRC Institute)."
BASE COUNT [illegible] a [illegible] c [illegible] g [illegible] t 2 others
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Matches [illegible]; Conservative [illegible]; Mismatches 2; Indels [illegible]; Gaps [illegible];

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[illegible]
Db [illegible] AGCGGATCC [illegible]

[illegible]
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DEFINITION [illegible] Soares NbHMPu S1 Homo sapiens cDNA clone IMAGE:1677645 [illegible] similar to [illegible] SUPPRESSOR [illegible] mRNA sequence.
ACCESSION AI[illegible]
VERSION AI[illegible].1 GI:[illegible]
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 46)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
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/organism "Homo sapiens"
/db_xref "taxon:9606"
/clone "IMAGE:1677645"
/clone_lib "Soares NbHMPu S1"
/tissue_type "Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host "DH10B"
/note "Organ: mixed (see below). Vector: [illegible] (Pharmacia) with a modified polylinker; Site [illegible]; Site 2: Eco RI; Equal amounts of plasmid DNA [illegible] normalized libraries (melanocyte 2NbHM, [illegible], NbHPU, and fetal heart NbHH19W) were mixed, [illegible] were made in vitro. Following HAP purification [illegible] was used as tracer in a subtractive hybridization reaction. The driver was PCR amplified cDNA [illegible] 5,000 clones made from the same 3 libraries [illegible] consisted of I.M.A.G.E. clones 200232 [illegible] [illegible] and [illegible]."
BASE COUNT [illegible] a [illegible] c [illegible] g [illegible] t
ORIGIN

Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches 14; Conservative 0; Mismatches 4; Indels [illegible];

Qy [illegible] AGCAGGATCCGCGA [illegible]
[illegible]
Db [illegible] AGCAGGATCCGGA 22

Search completed: July 17, 2003, 20:46:28
Job time : 1311 secs

[illegible]
Copyright (c) [illegible] Ltd.

[illegible] nucleic search, using sw model

Run on: July 17, 2003, 20:[illegible] ; Search time 36 Seconds
(without alignments)
[illegible] Million cell updates/sec

Title: US [illegible]
Perfect score: 20
Sequence: [illegible]

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: [illegible] seqs, [illegible] residues

[illegible] satisfying chosen parameters: [illegible]

Minimum DB seq length: [illegible]
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: [illegible] *
2: [illegible] *
3: [illegible] *
4: [illegible] *
5: [illegible] *
6: [illegible] *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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3	[illegible]	64.[illegible]	29	[illegible]	US 08 [illegible]	Sequence 55, Appl
4	[illegible]	[illegible]	[illegible]	[illegible]	US [illegible]	Sequence 6, Appli
5	[illegible]	[illegible]	[illegible]	[illegible]	US 08 [illegible]	Sequence 37, Appl
6	[illegible]	[illegible]	[illegible]	[illegible]	US 08 [illegible]	Sequence 29, Appl
7	[illegible]	[illegible]	[illegible]	1	US [illegible]	Sequence 240, App
8	[illegible]	[illegible]	[illegible]	1	US [illegible]	Sequence 9, Appli
9	[illegible]	[illegible]	[illegible]	1	US [illegible]	Sequence 37, Appl
10	[illegible]	[illegible]	[illegible]	1	US [illegible]	Sequence 50, Appl
11	[illegible]	[illegible]	[illegible]	[illegible]	US [illegible]	Sequence 44, Appl
12	[illegible]	[illegible]	[illegible]	1	US [illegible]	Sequence 44, Appl
13	[illegible]	[illegible]	[illegible]	[illegible]	US 08 [illegible]	Sequence 195, App
14	[illegible]	[illegible]	[illegible]	1	US [illegible]	Sequence 195, App
15	[illegible]	[illegible]	[illegible]	1	US [illegible]	Sequence 821, App
16	[illegible]	[illegible]	[illegible]	1	US 08 [illegible]	Sequence 28, Appl
17	[illegible]	[illegible]	[illegible]	[illegible]	US [illegible]	Sequence 28, Appl
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21	[illegible]	[illegible]	[illegible]	1	US [illegible]	Sequence 29, Appl
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ALIGNMENTS

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; Sequence 1178, Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
; APPLICANT: [illegible] Marta
; APPLICANT: Bouqueleret, Lydie
; APPLICANT: [illegible], Ilya
; APPLICANT: [illegible], Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC [illegible]
; [illegible] INVOLVED IN ARACHIDONIC ACID METAB[illegible]
; FILE REFERENCE: GENSET.051CP1
; CURRENT APPLICATION NUMBER: US/[illegible],641,[illegible]
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US [illegible]
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US [illegible]
; PRIOR FILING DATE: [illegible]
; PRIOR APPLICATION NUMBER: US [illegible]
; PRIOR FILING DATE: [illegible]
; PRIOR APPLICATION NUMBER: US [illegible]
; PRIOR FILING DATE: [illegible]
; NUMBER OF SEQ ID NOS: [illegible]
; SOFTWARE: Patent.pm
; SEQ ID NO 1178
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 21
; OTHER INFORMATION: [illegible] polymorphic base [illegible]
US [illegible]

Query Match [illegible]; Score [illegible]; DB 1; Length 17;
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]

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RESULT 2
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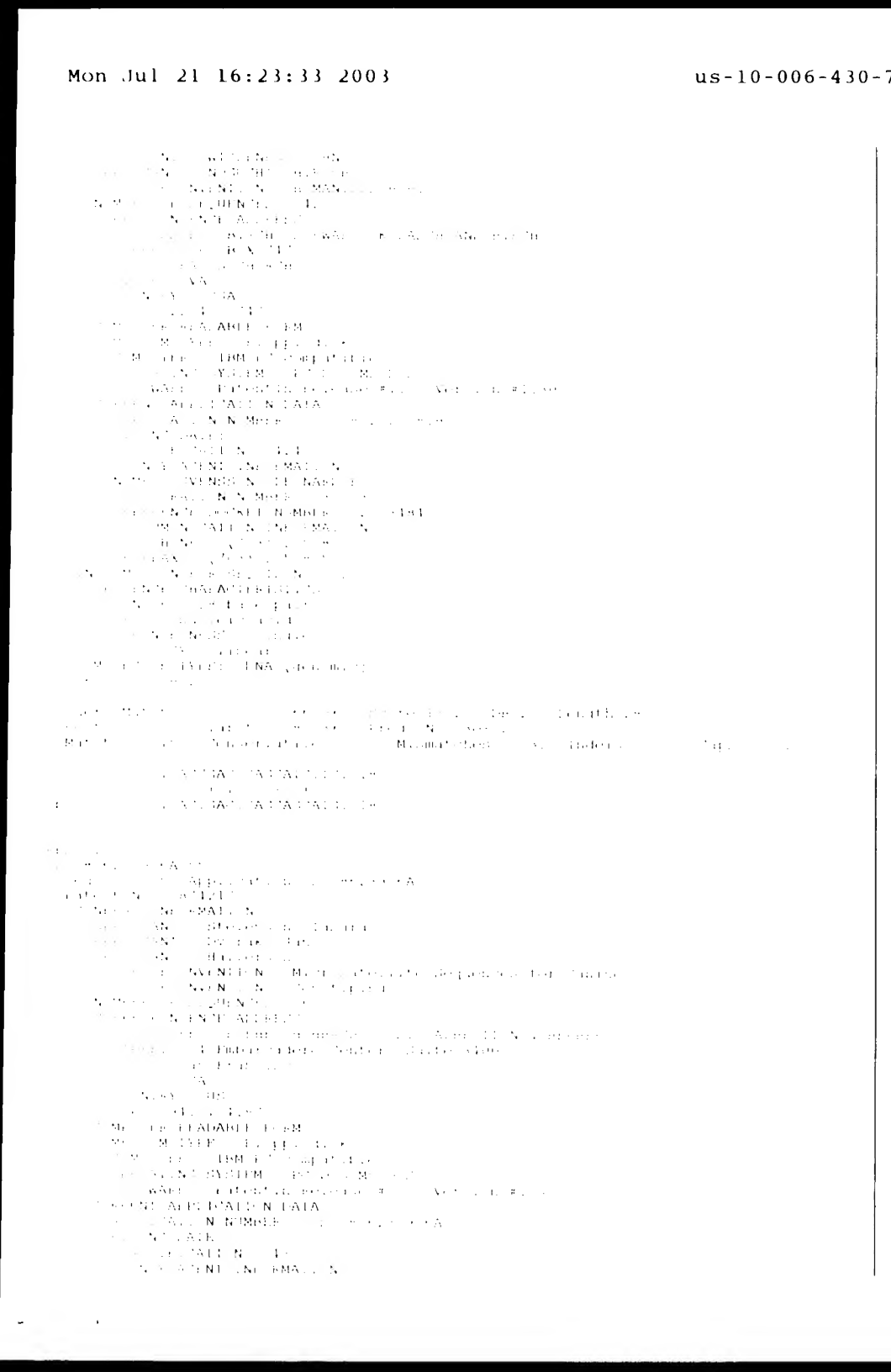
; Sequence 2[illegible], Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, [illegible]
; APPLICANT: GOMI, HIDEYUKI



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[illegible]
; Sequence [illegible], Application US/08/[illegible]A
; Patent No. [illegible]
; GENERAL INFORMATION:
;   APPLICANT: [illegible], Kim [illegible]
;   APPLICANT: [illegible], [illegible]
;   APPLICANT: Miller, Louis H.
;   APPLICANT: Peterson, David S.
;   APPLICANT: Su, Xin-zhuan
;   APPLICANT: Wellems, Thomas E.
;   TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
;   TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
;   NUMBER OF SEQUENCES: [illegible]
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Knobbe Martens Olson & Bear
;     STREET: [illegible] Newport Center Drive [illegible] Floor
;     CITY: Newport Beach
;     STATE: California
;     COUNTRY: US
;     ZIP: [illegible]
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/[illegible]A
;     FILING DATE: 07 DEC 1995
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Israelsen, Ned
;     REGISTRATION NUMBER: [illegible]
;     REFERENCE/DOCKET NUMBER: NIH[illegible]
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (619) 235-[illegible]
;     TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: [illegible]:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 30 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE:
;   ORIGINAL SOURCE:
[illegible]

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Best Local Similarity  87.5%;  Pred. No. [illegible];
Matches   14;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

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[illegible]
; Sequence [illegible], Application US/08/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;   APPLICANT: [illegible], Kim [illegible]
;   APPLICANT: [illegible], [illegible]
;   APPLICANT: Miller, Louis H.
;   APPLICANT: Peterson, David S.
;   APPLICANT: Su, Xin-zhuan
;   APPLICANT: Wellems, Thomas E.
;   TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
;   TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
;   NUMBER OF SEQUENCES: [illegible]
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Knobbe Martens Olson & Bear
;     STREET: [illegible] Newport Center Drive [illegible]
;     CITY: Newport Beach
;     STATE: California
;     COUNTRY: US
;     ZIP: [illegible]
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/[illegible]
;     FILING DATE: 10 SEP 1993
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Israelsen, Ned
;     REGISTRATION NUMBER: [illegible]
;     REFERENCE/DOCKET NUMBER: NIH[illegible]
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (619) [illegible]
;     TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: [illegible]:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 30 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE:
;   ORIGINAL SOURCE:
US-08-487-826B-[illegible]

Query Match          64.0%;  Score 12.8;  DB [illegible];  Length [illegible];
Best Local Similarity  87.5%;  Pred. No. [illegible];
Matches   14;  Conservative   0;  Mismatches   2;  Indels   [illegible]

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Db        [illegible] ATCAGAA[illegible]A [illegible]


RESULT [illegible]
US-09-358-972-240
; Sequence 240, Application US/09[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;   APPLICANT: Sh[illegible], [illegible] W
;   APPLICANT: Lewis, Martin K.
;   APPLICANT: Hoppe, Donna
;   APPLICANT: Mandrekar, Michelle
;   APPLICANT: Kephart, Daniel
;   APPLICANT: Rhodes, Richard B.
;   APPLICANT: Andrews, Christine A.
;   APPLICANT: Hartnett, James R.
;   APPLICANT: Gu, Trent
;   APPLICANT: Olson, Ryan J.
;   APPLICANT: Wood, Keith W.
;   APPLICANT: Welch, Roy
;   TITLE OF INVENTION: Nucleic Acid Detection
;   FILE REFERENCE: Pro [illegible] 6808/[illegible]
;   CURRENT APPLICATION NUMBER: US/09/[illegible]
;   CURRENT FILING DATE: 1999-07-2[illegible]
;   EARLIER APPLICATION NUMBER: 09/2[illegible]
;   EARLIER FILING DATE: 1999-02-18
;   EARLIER APPLICATION NUMBER: 09/042,287
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Db [illegible] CCAGTCAGGATCT 16

RESULT 11
US-08-559-038-44/c
; Sequence 44, Application US/08559038
; Patent No. 5804501
; GENERAL INFORMATION:
; APPLICANT: NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA
; APPLICANT: GRODEN
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT
; TITLE OF INVENTION: OF BLOOM'S SYNDROME
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
; STREET: 90 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE DISKETTE
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MS DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,038
; FILING DATE: NOVEMBER 15, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ELIZABETH A. BOGOSIAN
; REGISTRATION NUMBER: 39,911
; REFERENCE/DOCKET NUMBER: [illegible]
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-5995
; TELEFAX: (212) 286-0854 or 286-0082
; TELEX: IWX 710-581-4766
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: OTHER NUCLEIC ACID
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-559-038-44

Query Match 62.0%; Score 13.4; DB 1; Length 21;
Best Local Similarity 92.9%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCAGTCAGGATCT 15
Db [illegible] CCAGTCAGGATCT 2

RESULT 12
US-09-175-828-44/c
; Sequence 44, Application US/09175828
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA
; APPLICANT: GRODEN
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT
; TITLE OF INVENTION: OF BLOOM'S SYNDROME
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
; STREET: 90 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE DISKETTE
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MS DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/175,828
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,303
; FILING DATE: NOVEMBER 15, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ELIZABETH A. BOGOSIAN
; REGISTRATION NUMBER: 39,911
; REFERENCE/DOCKET NUMBER: [illegible]
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-5995
; TELEFAX: (212) 286-0854 or 286-0082
; TELEX: IWX 710-581-4766
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: OTHER NUCLEIC ACID
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-09-175-828-44

Query Match 62.0%; Score 13.4; DB 4; Length 21;
Best Local Similarity 92.9%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCAGTCAGGATGT 15
Db 15 CTCAGTCAGGATGT 2

RESULT 13
US-08-859-998-195
; Sequence 195, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvilli, Robert
; TITLE OF INVENTION: METHODS OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95

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Run on: Search, using sw model

Run time: July 17, 2003, 20:06:52 ; Search time 115 Seconds
(without alignments)
78.793 Million cell updates/sec

Title: US-10-006-430-76
Perfect score: 20
Sequence: 1 acggaccaggaatggtgtga 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1149767 seqs, 1031500326 residues

Total number of hits satisfying chosen parameters: 91414

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications NA:*
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13: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, estimated by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match	Length	DB	ID	Description
	1	100.0	20	15	US-10-006-430-76		Sequence 76, Appl
	2	67.0	25	15	US-10-098-263B-117442		Sequence 117442,
	3	67.0	31	10	US-09-861-273-1445		Sequence 1445, Ap
	4	65.0	25	15	US-10-098-263B-55507		Sequence 55507, A
	5	64.0	17	12	US-09-877-428-200		Sequence 200, App
	6	64.0	17	12	US-09-877-428-901		Sequence 901, App
	7	64.0	18	11	US-09-964-373-1732		Sequence 1732, Ap
	8	64.0	25	15	US-10-215-112-5569		Sequence 5569, Ap
	9	64.0	25	15	US-10-098-263B-27690		Sequence 27690, A
	10	64.0	25	15	US-10-098-263B-69440		Sequence 69440, A
	11	64.0	25	15	US-10-098-263B-81262		Sequence 81262, A
	12	64.0	25	15	US-10-098-263B-113668		Sequence 113668,
	13	64.0	30	12	US-09-764-417-240		Sequence 240, App
	14	64.0	8	15	US-10-153-274-47		Sequence 47, Appl
	15	64.0	31	12	US-09-941-263-97		Sequence 97, Appl
	16	64.0	25	15	US-10-098-263B-11446		Sequence 11446, A
	17	62.6	63.0	25	15	US-10-098-263B-17508	Sequence , A
	18	62.6	63.0	25	15	US-10-098-263B-60520	Sequence , A
	19	62.6	63.0	25	15	US-10-098-263B-105128	Sequence ,
	20	62.6	63.0	25	15	US-10-098-263B-116073	Sequence ,
	21	62.6	63.0	25	15	US-10-098-263B-127368	Sequence ,
C	22	62.1	62.0	21	11	US-09-754-141-44	Sequence ,
	23	62.4	62.0	25	15	US-10-098-263B-44418	Sequence ,
C	24	62.2	61.0	17	12	US-09-877-428-201	Sequence ,
C	25	62.2	61.0	25	15	US-10-098-263B-16257	Sequence ,
C	26	62.2	61.0	25	15	US-10-098-263B-16258	Sequence ,
C	27	62.2	61.0	25	15	US-10-098-263B-52009	Sequence ,
C	28	62.2	61.0	25	15	US-10-098-263B-73679	Sequence ,
	29	62.2	61.0	25	15	US-10-098-263B-76127	Sequence ,
C	30	62.2	61.0	25	15	US-10-098-263B-127560	Sequence ,
	31	62.2	61.0	33	10	US-09-759-143-821	Sequence ,
	32	62.2	61.0	33	10	US-09-780-669-821	Sequence ,
	33	62.2	61.0	33	10	US-09-822-827-821	Sequence ,
	34	62.2	61.0	33	11	US-09-895-793-821	Sequence ,
	35	62.2	61.0	33	11	US-09-895-814-821	Sequence ,
	36	62.2	61.0	33	15	US-10-012-896-821	Sequence ,
C	37	62.2	61.0	34	11	US-09-741-106-28	Sequence ,
C	38	62.2	61.0	35	12	US-09-862-894A-8	Sequence ,
	39	62.2	61.0	36	11	US-09-741-106-29	Sequence ,
	40	62.2	61.0	38	12	US-09-730-289B-2834	Sequence ,
	41	62.2	61.0	38	12	US-09-930-423-3202	Sequence ,
	42	62.2	61.0	42	15	US-10-022-832-42	Sequence ,
	43	12	60.0	25	15	US-10-098-263B-29872	Sequence ,
	44	12	60.0	25	15	US-10-098-263B-49021	Sequence ,
C	45	12	60.0	25	15	US-10-098-263B-87719	Sequence ,

ALIGNMENTS

RESULT 1
US-10-006-430-76
; Sequence 76, Application US/10006430
; Publication No. US20030104110A1
; GENERAL INFORMATION:
; APPLICANT: Mark J. Graham
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF [illegible] EXPRESSION
; FILE REFERENCE: RTS-0341
; CURRENT APPLICATION NUMBER: US/10/006,430
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ IDS: 90
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-006-430-76

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 20; Conservative 0; Mismatches 0; Indels 0;

Qy 1 acggaccaggaatggtgtga 20
||||||||||||||||||||
Db 1 acggaccaggaatggtgtga 20

RESULT 2
US-10-098-263B-117442
; Sequence 117442, Application US/10098263B
; Publication No. US20030104110A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 4118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08

RESULT 5
US/09/877,178/pn/2
; Sequence 2, Application: US/09/877,178
; Publication No.: US20020086347A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Edith
; TITLE OF INVENTION: Methods and Reagents for Inhibition of Hepatitis B Virus Replication
; FILE REFERENCE: MRIBO-037 B (100/029)
; CURRENT APPLICATION NUMBER: US/09/877,178
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 60/215,102
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/215,103
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/215,104
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/215,105
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/215,106
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/215,107
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/215,108
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/215,109
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1
; TYPE: DNA
; ORGANISM: Hepatitis B virus
US/09/877,178/pn/2

RESULT 6
US/09/877,178/pn/3
; Sequence 3, Application: US/09/877,178
; Publication No.: US20020086347A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Edith
; TITLE OF INVENTION: Methods and Reagents for Inhibition of Hepatitis B Virus Replication
; FILE REFERENCE: MRIBO-037 B (100/029)
; CURRENT APPLICATION NUMBER: US/09/877,178
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 60/215,102
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/215,103
; PRIOR FILING DATE: 2000-06-30

; APPLICATION NUMBER: US 09/636,385
; FILING DATE: 2000-08-09
; APPLICATION NUMBER: US 09/636,447
; FILING DATE: 2000-10-24
; APPLICATION NUMBER: US 08/193,627
; FILING DATE: 1994-02-07
; APPLICATION NUMBER: US 08/443,995
; FILING DATE: 1995-05-04
; APPLICATION NUMBER: US 08/434,504
; FILING DATE: 1995-05-04
; APPLICATION NUMBER: US 09/436,430
; FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6011
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Hepatitis A virus
; FEATURE:

Query Match 64.0%; Score 12.8; DB 12; Length 17;
Best Local Similarity 87.5%; Prod. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGGAGTCAGGATGTTGT 18
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Db 2 CGACTCAAGATGTTGT 17

; SEQ ID NO 12562
; Sequence 12562, Application US/09999373
; Publication No. US20020136852A1
; GENERAL INFORMATION:
; APPLICANT: Ellerby, Roger L.
; APPLICANT: Hanby, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 08-1052-0A
; CURRENT APPLICATION NUMBER: US/09/999,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 09/805,760
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 45994
; SEQ ID NO 12562
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:

Query Match 64.0%; Score 12.8; DB 11; Length 18;
Best Local Similarity 87.5%; Prod. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGGAGTCAGGATGTTGT 18
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Db 2 CGACTCAGGATGCTGT 17

; SEQ ID NO 5569
; Sequence 5569, Application US/10215112
; Publication No. US20030087500A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes
; TITLE OF INVENTION: Test 5
; FILE REFERENCE: 4119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5569
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-215-112-5569

Query Match 64.0%; Score 12.8; DB 15; Length 25;
Best Local Similarity 87.5%; Prod. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGGAGTCAGGATGTTGT 18
||| ||| ||||||| |
Db 4 CGACTCAGCATGTTGT 19

RESULT 9
US-10-098-263B-27690/c
; Sequence 27690, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 4118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 27690
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-27690

Query Match 64.0%; Score 12.8; DB 15; Length 25;
Best Local Similarity 87.5%; Prod. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACGGAGTCAGGATGTT 16
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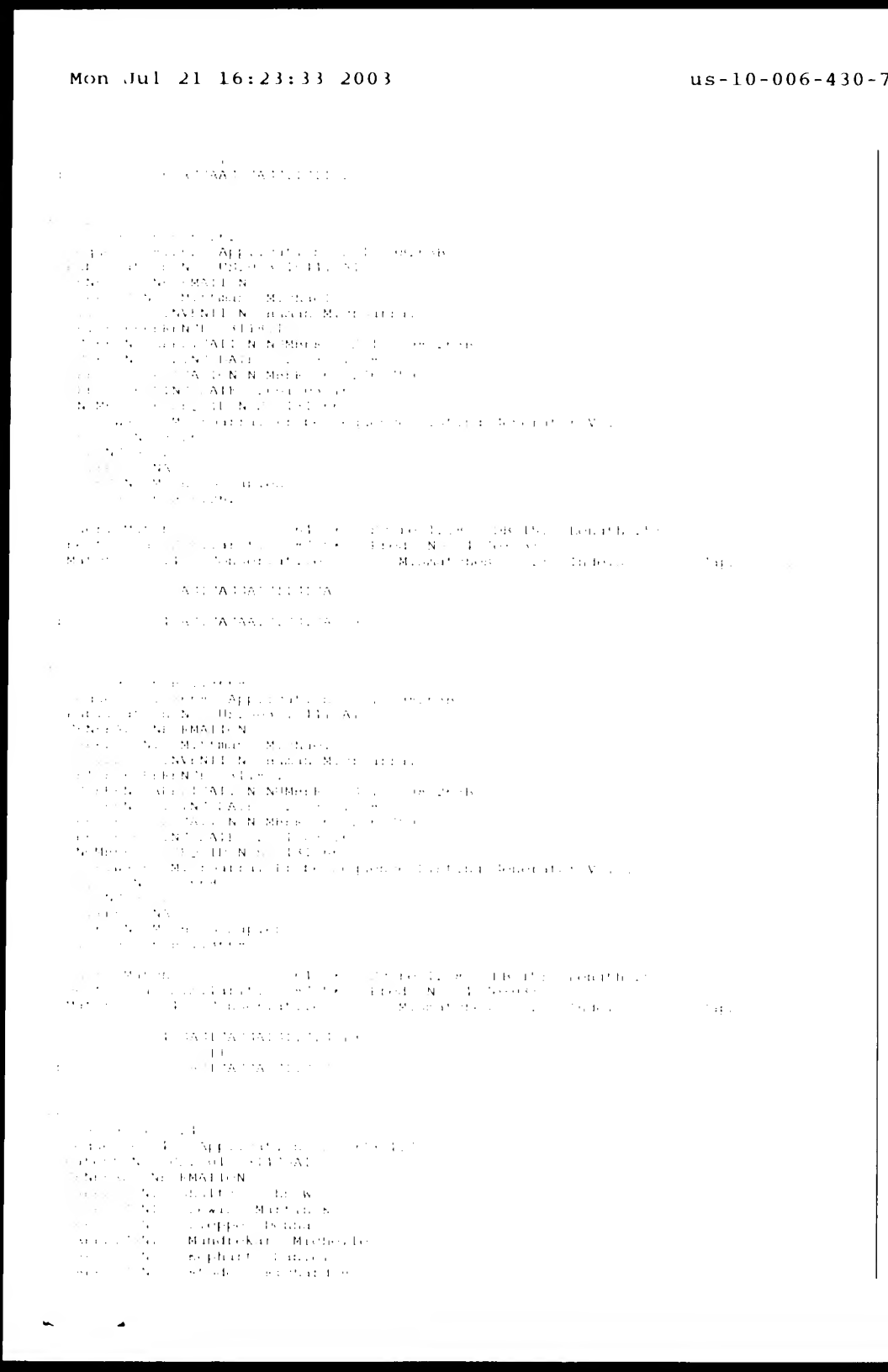
Db 22 ACGGAGTCAGAATTT 7

RESULT 10
US-10-098-263B-69440
; Sequence 69440, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 4118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 69440
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-69440

Query Match 64.0%; Score 12.8; DB 15; Length 25;
Best Local Similarity 87.5%; Prod. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACGGAGTCAGGATGTT 16



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Copyright (c) [illegible]

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[illegible] 1496

[illegible]

Database : [illegible]

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match	Length	DB	ID	Description
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	4	[illegible]	[illegible]	547	11	[illegible]07198	[illegible]
	5	4[illegible]	[illegible]	[illegible]	9	AF[illegible]	[illegible]
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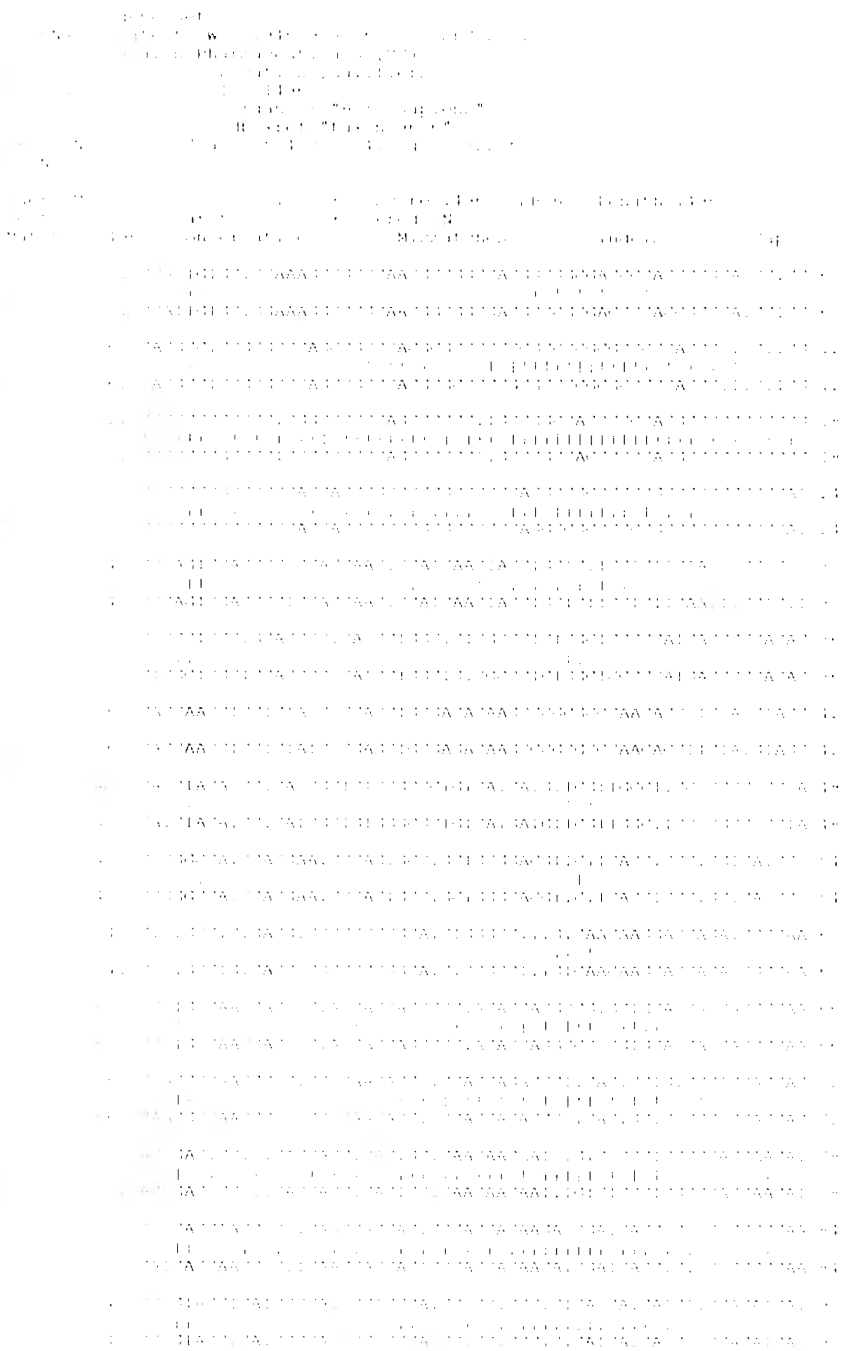
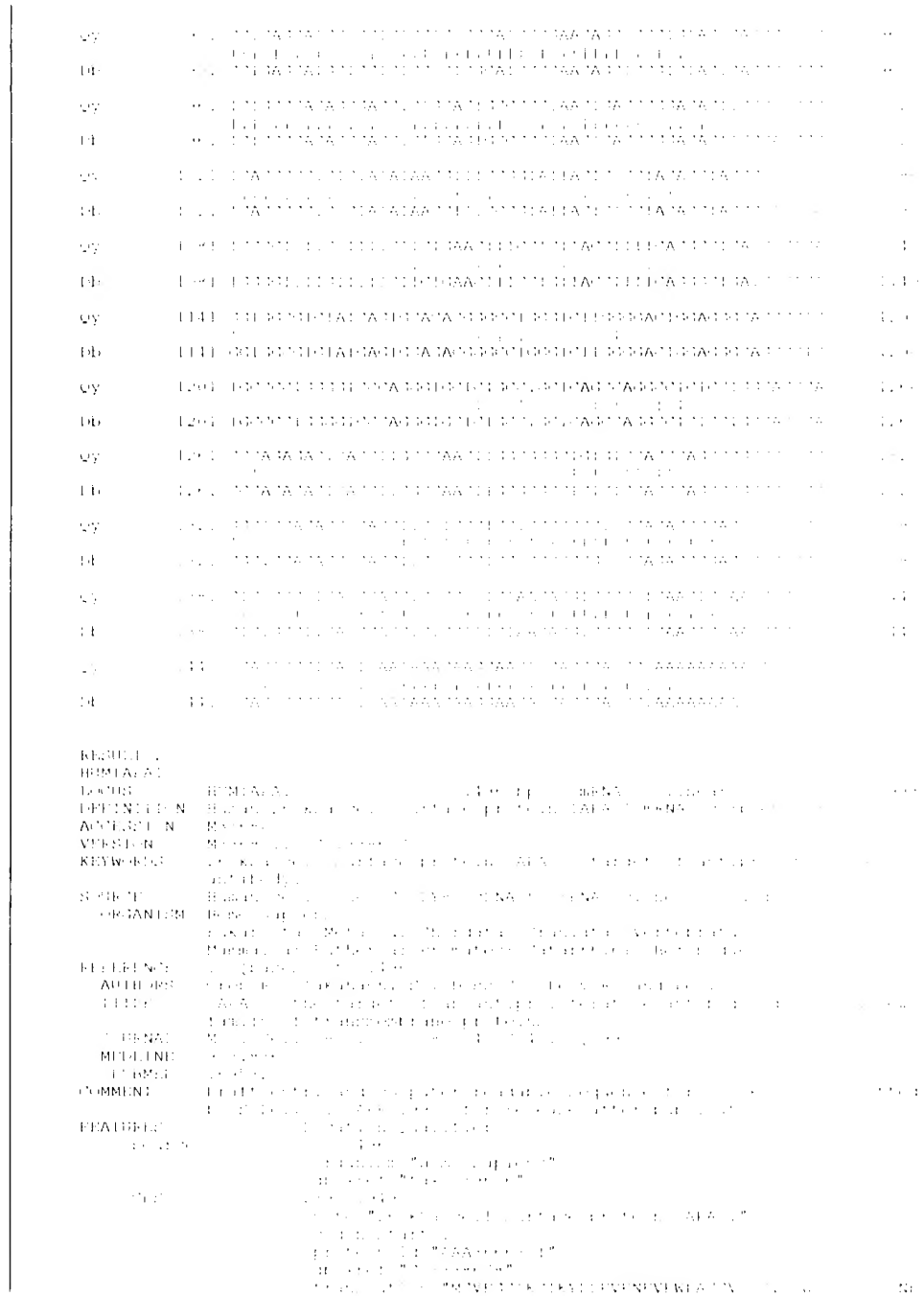
	7	421	28.[illegible]	[illegible]	[illegible]	A[illegible]	[illegible]
c	8	424	28.[illegible]	1[illegible]748	2	AC0[illegible]012	[illegible]
	9	421	28.[illegible]	[illegible]	2	A[illegible]	[illegible]
c	10	317	21.2	429	6	AX108983	[illegible]
c	11	[illegible]	[illegible]	[illegible]	[illegible]	AX[illegible]	[illegible]
c	12	31[illegible]	20.8	311	6	AX062746	[illegible]
c	13	31[illegible]	[illegible]	[illegible]	6	AX[illegible]	[illegible]
	14	273	18.2	[illegible]	6	AX004409	[illegible]
	15	[illegible]	[illegible]	[illegible]	6	AX[illegible]	[illegible]
c	16	18[illegible]	12.[illegible]	274	6	AX[illegible]	[illegible]
c	17	1[illegible]	11.[illegible]	[illegible]	[illegible]	AX[illegible]	[illegible]
	18	171	11.4	257	6	AX209343	[illegible]
	19	1[illegible]	11.1	[illegible]	[illegible]	AX[illegible]	[illegible]
	20	141	9.4	140[illegible]77	9	AC002536	[illegible]
	21	11[illegible]	[illegible]	[illegible]	[illegible]	AX[illegible]	[illegible]
	22	107	7.2	711	9	SOE250197	[illegible]
	23	104	[illegible]	[illegible]	9	AF[illegible]	[illegible]
	24	83	5.5	311	6	AX396242	[illegible]
c	25	[illegible]	[illegible]	[illegible]	2	A[illegible]	[illegible]
	26	77	5.1	711	9	AF116599	[illegible]
c	27	[illegible]	4.[illegible]	[illegible]	6	AX4[illegible]	[illegible]
	28	54	3.6	138229	2	HSAC001236	[illegible]
	29	[illegible]	[illegible]	[illegible]	10	S44[illegible]	[illegible]
	30	53	3.5	1234	10	MMMB3MRN	[illegible]
	31	[illegible]	3.5	[illegible]	10	[illegible]	[illegible]
	32	53	3.5	1510	10	[illegible]011433	[illegible]
c	33	[illegible]	3.5	[illegible]	10	AF[illegible]	[illegible]
	34	53	3.5	213[illegible]41	2	AC015800	[illegible]
c	35	[illegible]	3.[illegible]	24[illegible]	10	MM[illegible]	[illegible]
c	36	53	3.5	249487	10	MMU25[illegible]	[illegible]
	37	4[illegible]	3.[illegible]	[illegible]	2	AC[illegible]	[illegible]
	38	46	3.1	123302	2	AC[illegible]	[illegible]
c	39	4[illegible]	3.1	[illegible]	[illegible]	AC[illegible]	[illegible]
	40	42	2.8	276	10	S4[illegible]	[illegible]
	41	[illegible]	[illegible]	[illegible]	1[illegible]	S4[illegible]	[illegible]
c	42	3[illegible]	2.2	[illegible]	10	AF[illegible]	[illegible]
	43	[illegible]	[illegible]	[illegible]	2	AC[illegible]	[illegible]
c	44	31	2.1	[illegible]	10	[illegible]	[illegible]
	45	[illegible]	[illegible]	[illegible]	[illegible]	AX[illegible]	[illegible]

ALIGNMENTS

RESULT 1
AX337094
LOCUS AX[illegible] [illegible] DNA [illegible]
DEFINITION Sequence [illegible] from Patent WO[illegible].
ACCESSION AX[illegible]
VERSION AX[illegible]
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS [illegible]
TITLE [illegible]





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                    EMILSMVL[illegible]NSSVY"
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[illegible]

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Db          1 [illegible]CATTGTGCTGGAAA[illegible]AAC[illegible]GACGGCGGACCCACCGGCATCCTGC 60

Qy         61 [illegible]GACCCTTTCTTCG 120
Db         61 [illegible]GACCCTTTCTTCG 120

Qy        121 [illegible] 180
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Qy        181 [illegible] 240
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Qy        301 [illegible] 360
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Qy        361 [illegible] 420
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Qy        421 [illegible] 480
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Qy        481 [illegible] 540
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Qy        601 [illegible] 660
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Qy        781 [illegible] 840
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Qy        841 [illegible] 900
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Qy        901 [illegible] 960
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DEFINITION  Homo sapiens, CD81 antigen (target of antiproliferative [illegible]
            1), clone MGC:2221 IMAGE:3510634, mRNA, complete cds.
ACCESSION   BC002978
VERSION     BC002978.1  GI:12804238
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; [illegible]
REFERENCE   1  (bases 1 to 1333)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-FEB-2001) National Institutes of Health, [illegible]
            Gene Collection (MGC), Cancer Genomics Office, National [illegible]
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD [illegible]
            USA
  REMARK    NIH MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield[illegible]
            Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland[illegible]
            Letticia Hsiao, Martin Krzywinski, Reta Kutsche, [illegible]
            Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy[illegible]
            Ness, Pawan Pandoh, Anna Liisa Prabhu, Parvaneh Saeedi[illegible]
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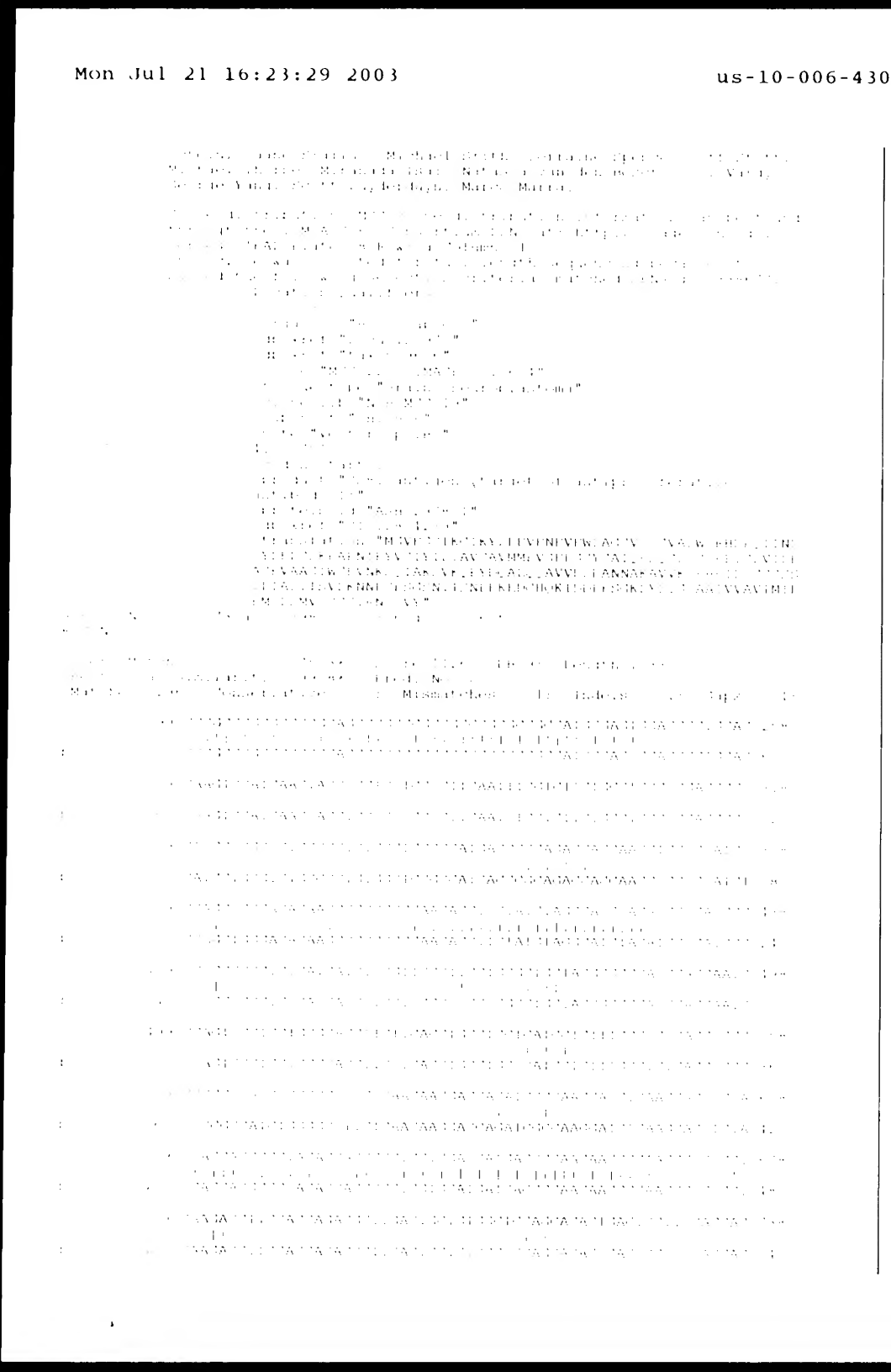

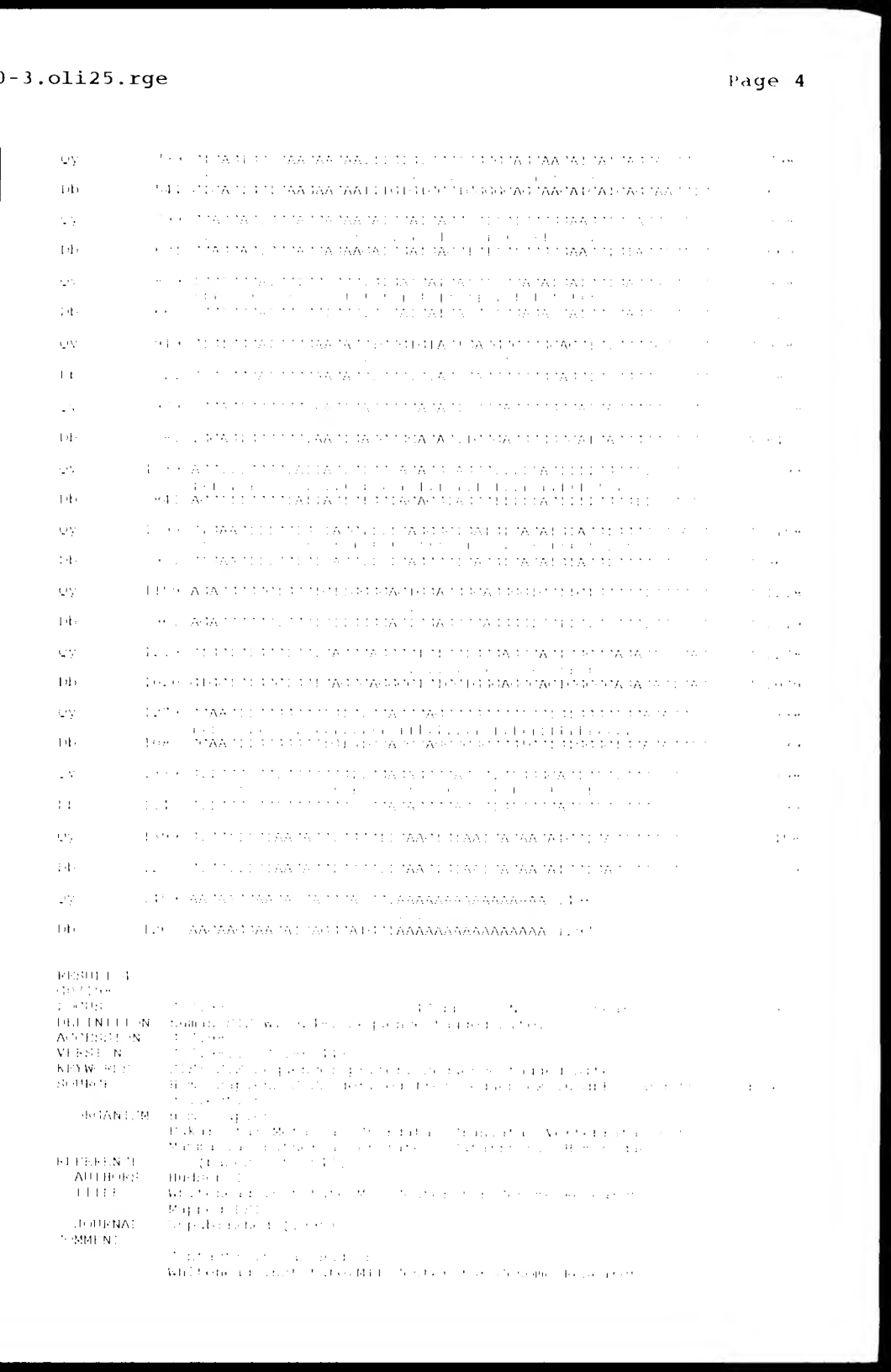

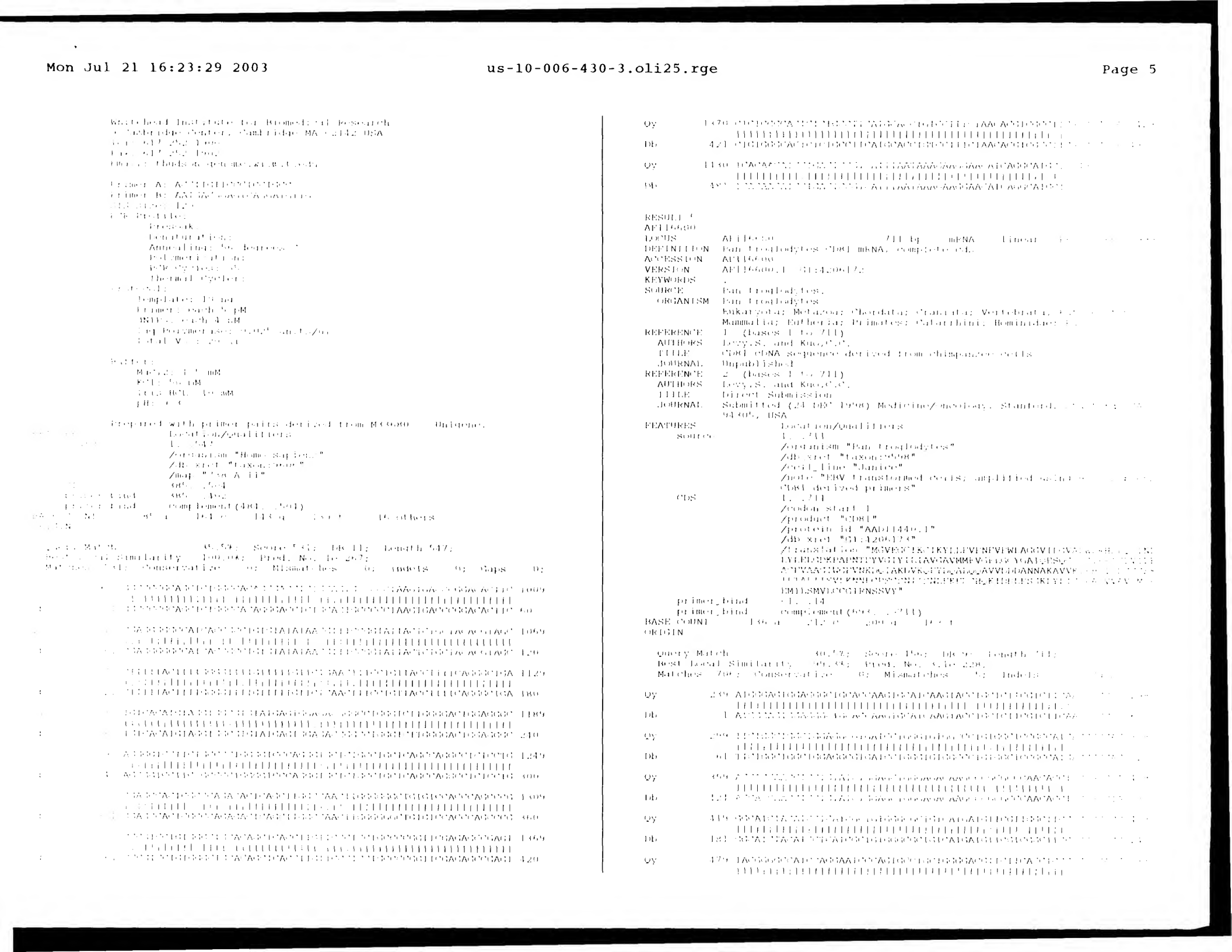

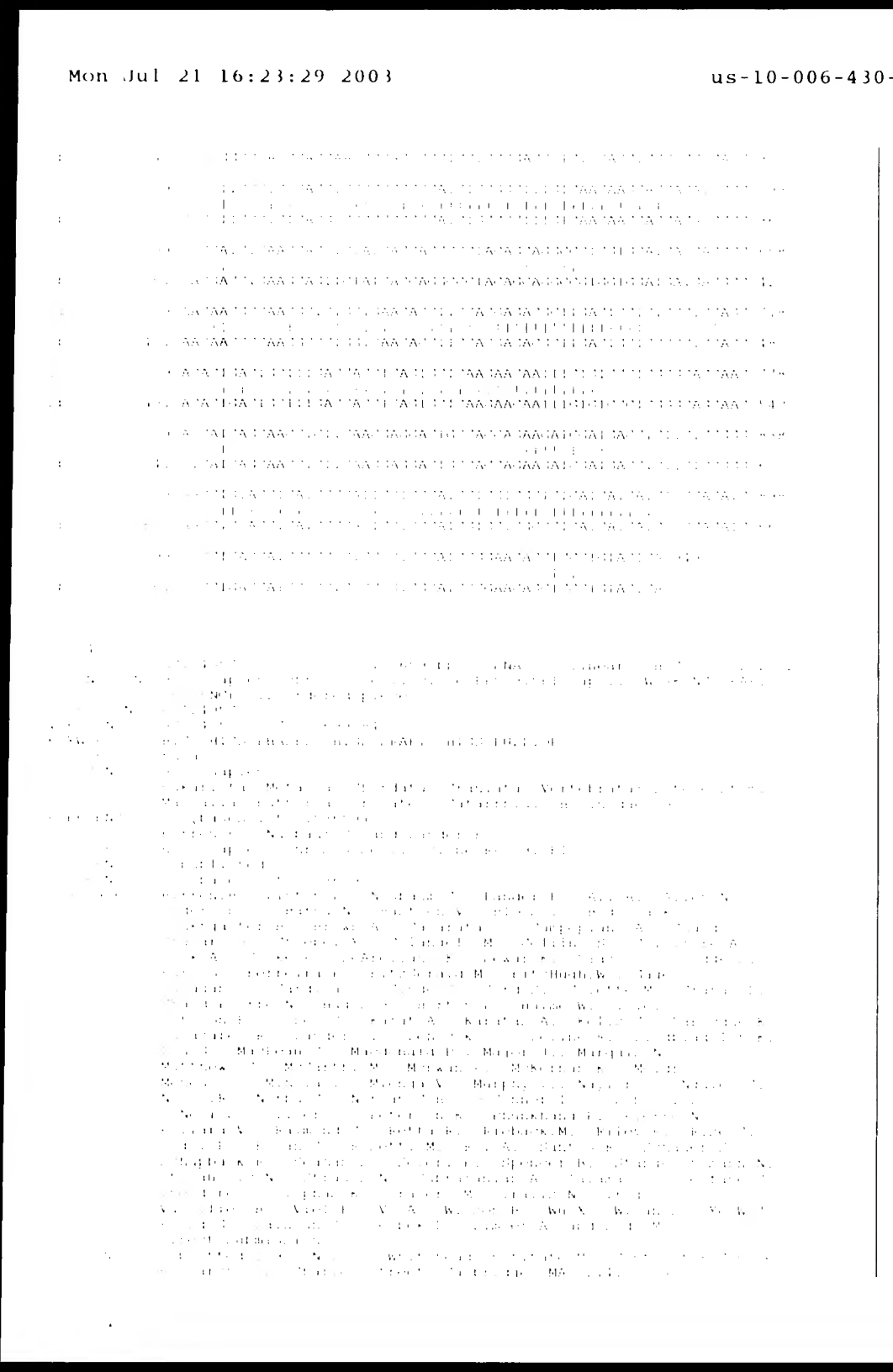

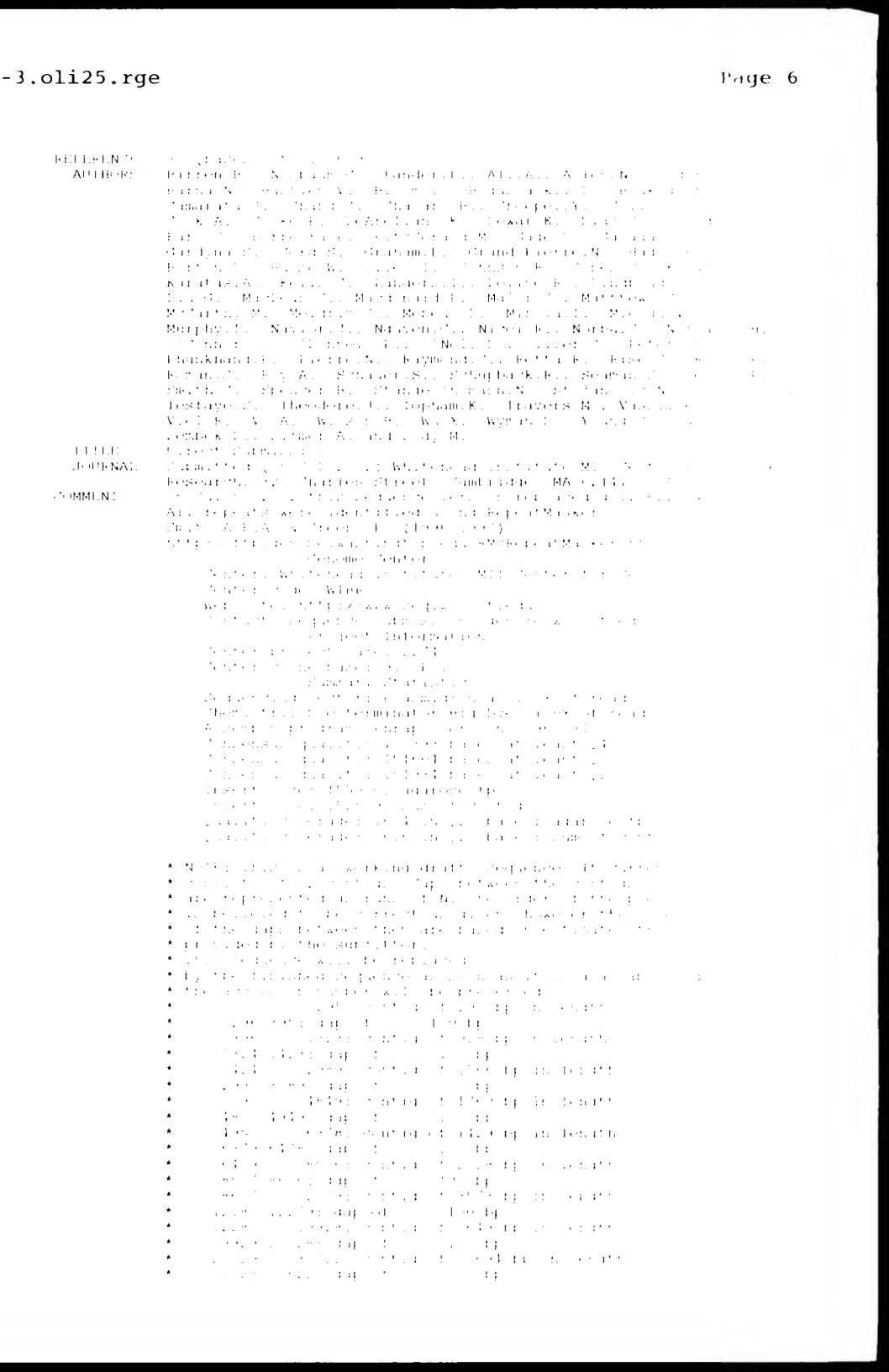

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     *     76436   76535: gap of        100 bp
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     *    109134  109233: gap of        100 bp
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                     /map="11"
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                     /clone_lib="RP5 Human (A) library 5"
     misc_feature    1..[illegible]
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BASE COUNT    42326 a  42054 c  42580 g  [illegible] t   1100 others
ORIGIN

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Db     [illegible] [illegible] 141554

Qy        [illegible] [illegible] 1005
Db     [illegible] [illegible] 141494

Qy        [illegible] [illegible] 1065
Db     [illegible] [illegible] 141434

Qy        [illegible] [illegible] 1125
Db     [illegible] [illegible] 141374

Qy        [illegible] [illegible] 1185
Db     [illegible] [illegible] 141314

Qy        [illegible] [illegible] 1245
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Qy        [illegible] [illegible] 1305
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Qy        [illegible] [illegible] 1365
Db     141194 [illegible]

Qy       1366 GAGTCTGTGGGCACTCTCTGCCTTCATGCACCTGTCTTCTAACA[illegible]
Db     141134 GAGTCTGTGGGCACTCTCTGCCTTCATGCACCTGTCTTCTAACA[illegible]

Qy       1426 [illegible]AAAAAAAAAAACATCAGGCA[illegible]
Db     141074 [illegible]ATTAAAAAAAAAAAACATCAGGCA[illegible]


RESULT 7
AC003693
LOCUS       AC003693               155074 bp    DNA     linear   [illegible]
DEFINITION  Human Chromosome 11p15.5 PAC clone pDJ915f1 containing [illegible]
            complete sequence.
ACCESSION   AC003693
VERSION     AC003693.1  GI:3687269
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; [illegible]
REFERENCE   1  (bases 1 to 155074)
  AUTHORS   Evans,G.A., Athanasiou,M., Amaya,P., Armstrong,D., [illegible]
            Buettner,J., Bumeister,R., Card,P., deSailboat,F., [illegible]
            English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M. [illegible]
            Grant,O., Hahner,L., Joslin,J., Lewis,E., Loo,H., [illegible]
            Major,L., McFarland,[illegible], Newton,J., Osborne Lawrence,S.
            Schageman,J., Schultz,R.A., Stimson,S., Syed,M. and [illegible]
  TITLE     HTGS Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 155074)
  AUTHORS   Evans,G.A., Athanasiou,M., Basit,M., Bradbury,P., [illegible]
            Bumesiter,R., Davis,C., English,C., Franklin,L., [illegible]
            Gee,V., Gordon,M., Gotway,G., Grant,O., Hahner,L., [illegible]
            Hinson,S., Narayanaswamy,[illegible], Newton,J., O'Brien,K., [illegible]
            Schageman,J., Schilling,P., Schultz,R., Syed,M., [illegible]
            Ward,T. and Wilson,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-1997) Genome Science & Technology, [illegible]
            University of Texas Southwester Medical Center, [illegible]
            Blvd, Dallas, TX 75235-8591, USA
REFERENCE   3  (bases 1 to 155074)
  AUTHORS   Evans,G.A., Athanasiou,M., Amaya,[illegible], Armstrong,[illegible]
            Buettner,J., Butler,C., Card,P., deSailboat,F., Dunn,
            English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M. [illegible]
            Grant,O., Hahner,L., Joslin,J., Lewis,E., Loo,H., [illegible]
            Major,L., McFarland,[illegible], Newton,J., Osborne Lawrence,[illegible]
            Schageman,J., Schultz,R.A., Stimson,S., Waller,K. and [illegible]
  TITLE     Direct Submission
  JOURNAL   Submitted (30-SEP-1998) Genome Science & Technology, [illegible]
            University of Texas Southwestern Medical Center, [illegible]
            Blvd, Dallas, TX 75235-8591, USA
COMMENT     On Oct 1, 1998 this sequence version replaced gi:[illegible]
            Further information regarding the map of this region [illegible]
            annotation of pDJ915f1 can be found at
            http://gestec.swmed.edu/chromoso.htm
            IMPORTANT: This submission contains the entire insert [illegible]
            pDJ915f1. pDJ915f1 comes from the RPCI-5 PAC library [illegible]
            at the Roswell Park Cancer Institute by the Pieter de [illegible]
            This clone has been finished according to strict qual[illegible]
            and attempts have been made to resolve all base ca[illegible]
            such as compressions and repetitive elements. The [illegible]
            Phred/Phrap calculated error/10kb is 0.0[illegible]. In addit[illegible]
            have been made to assure over 99% of consensus base[illegible]
            of either double stranded coverage or 2 types of lab[illegible]
            on one strand.
            CHROMOSOMAL LOCUS: This PAC clone comes from the [illegible]
            Wilms tumor type 2 (WT2) region between ESTs CTSD and [illegible]
            This region spanning approximately 2 Mbp is mapped to [illegible]
            and D11S12[illegible].
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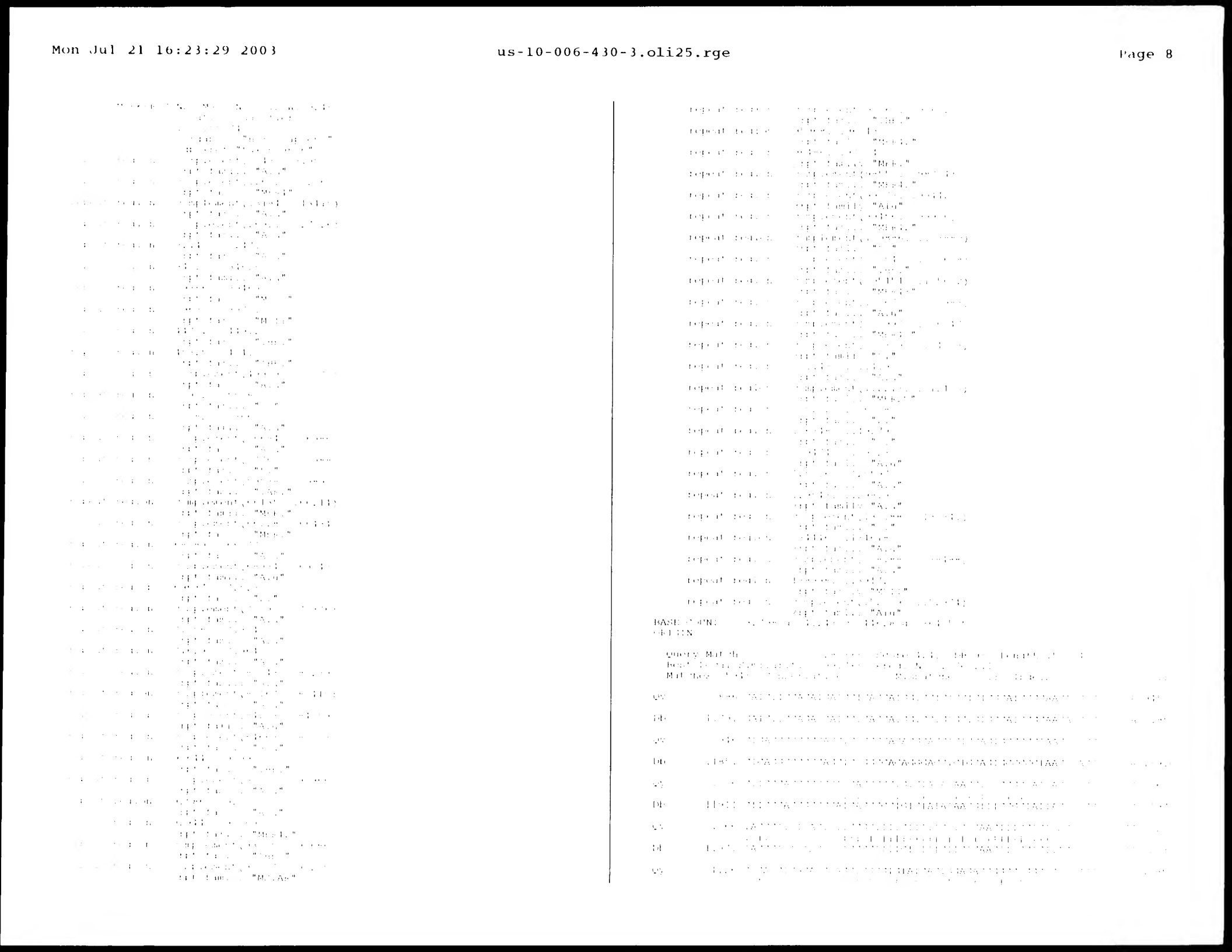

[illegible sequence alignment lines]

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[illegible]
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 159718)
[illegible], Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-113A6
Unpublished
(bases 1 to 159718)
Birren, B., [illegible], Nusbaum, C., Lander, E., Allen, N., Anderson, S., [illegible], N., Bastien, V., Bogoslavskiy, I., Boukhgalter, B., Brown, A., [illegible] ... [illegible] ... Graham, L., ... Horton, L., Holmes, W., ... Matthews, C., McCarthy, M., ... Mcpherson, ... Meneus, L., ... Nguyen, C., Norbu, C., ... O'Neill, D., Oliver, J., ... Raymond, C., ... Seaman, S., ... Stange-Thomann, N., ... Testaye, S., ... Vassiliev, H., ... Zody, M.
Direct Submission
Submitted (14 MAR 2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
(bases 1 to 159718)
Birren, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S., [illegible] ... Boukhgalter, B., ... Dewar, K., ... Graham, L., ... Holmes, W., ... Jones, C., Kamat, A., ... Lander, E., [illegible]

[illegible], Macdonald, P., Major, J., Matthews, McCarthy, M., ... Meneus, L., ... Murphy, L., Naylor, J., Nguyen, C., ... Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., ... Raymond, C., ... Roman, J., ... Seaman, S., ... Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., ... Testaye, S., Theodore, J., Topham, K., Travers, M., ... Wilson, B., Wu, X., ... Zembek, L., Zimmer, A. and Zody, M.

TITLE Direct Submission
JOURNAL Submitted (15 AUG 2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Aug 15, 2002 this sequence version replaced [illegible]. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L11782
Center clone name: 113_A_6

* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 3456: contig of 3456 bp in length
* 3457 3556: gap of 100 bp
* 3557 7167: contig of 3611 bp in length
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* [illegible]: contig of [illegible] bp in length
* 63687 63786: gap of 100 bp
* [illegible]: contig of [illegible] bp in length
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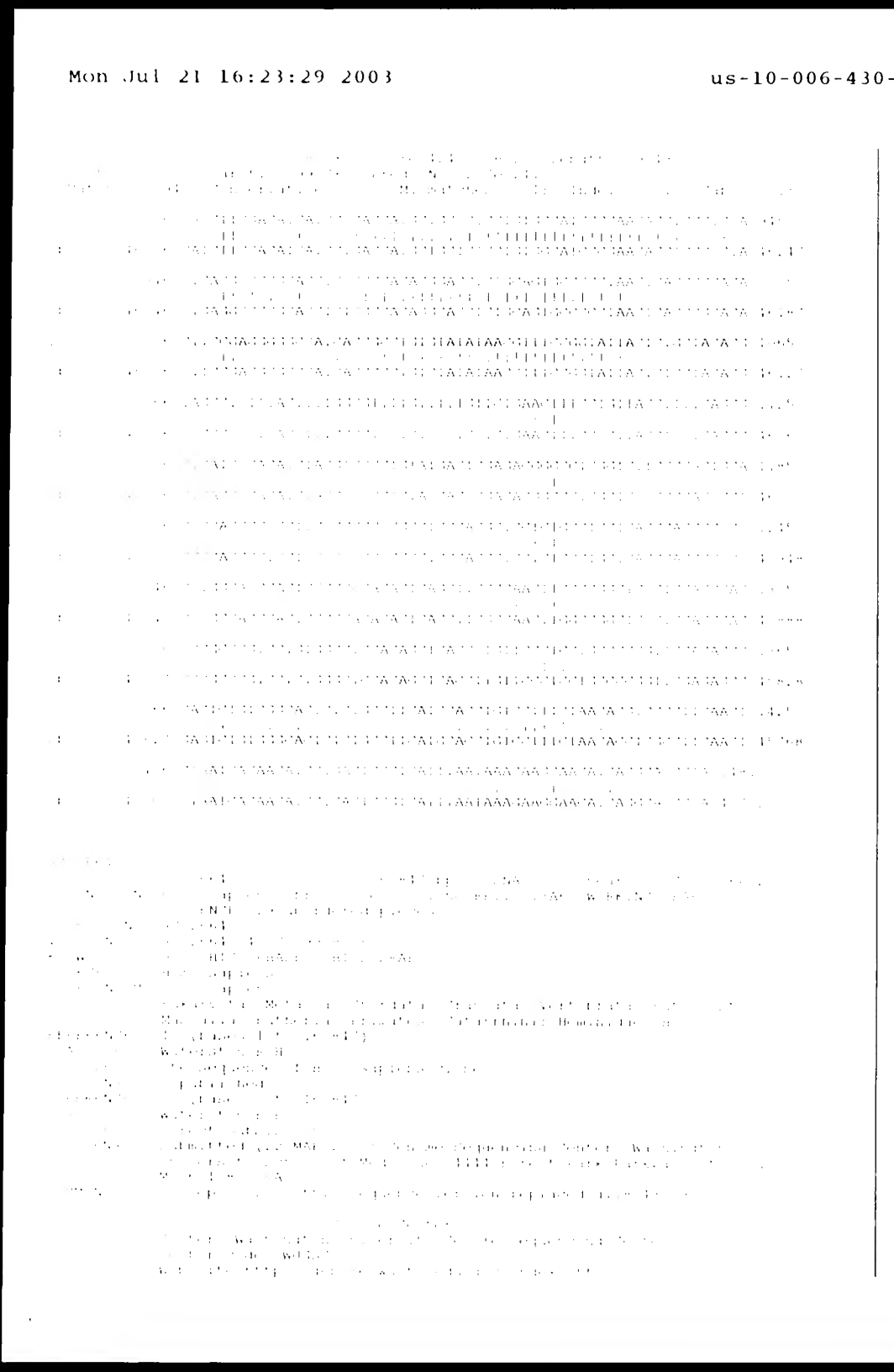

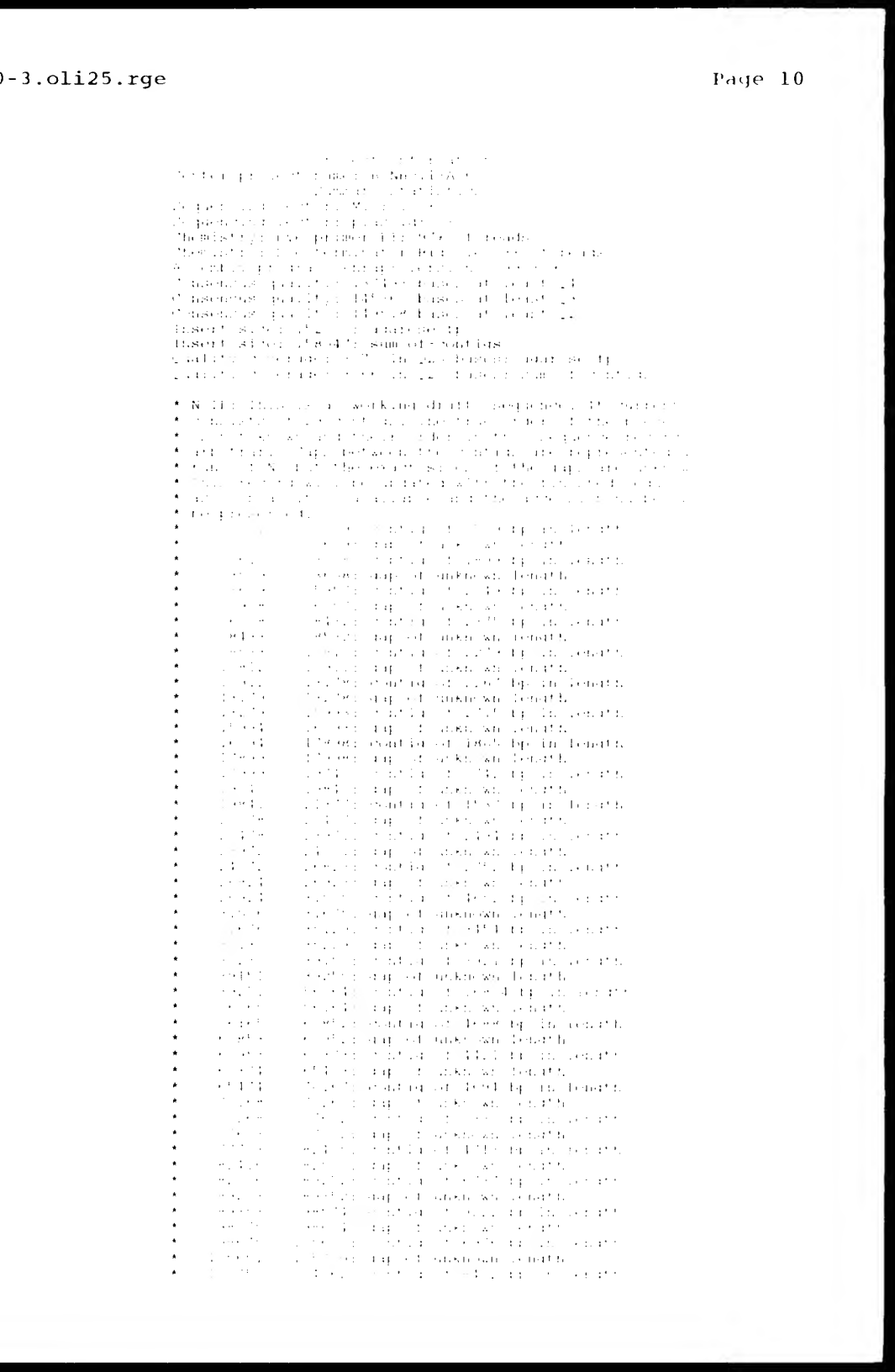

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ORIGIN

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  Best Local Similarity   99.7%;  Pred. No. 2.7e-211;
  Matches  594;  Conservative    0;  Mismatches    1;  Indels    [illegible];  Gaps    [illegible];

Qy        [illegible]
Db     [illegible]

Qy        [illegible]
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Qy        [illegible]
Db     [illegible]

Qy       1066 [illegible]
Db     128253 [illegible]

Qy       1126 [illegible]
Db     128313 [illegible]

Qy       1186 [illegible]
Db     128373 [illegible]

Qy       1246 [illegible]
Db     [illegible]

Qy       1306 [illegible]
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Qy       1366 [illegible]
Db     128552 [illegible]

Qy       1426 [illegible]
Db     [illegible]


RESULT 13
AX198983/c
LOCUS       AX198983                 429 bp    DNA     linear   PAT [illegible]
DEFINITION  Sequence 1138 from Patent WO0151513.
ACCESSION   AX198983
VERSION     AX198983.1  GI:15389[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; [illegible]
REFERENCE   1  (bases 1 to 429)
  AUTHORS   Algate,P.A.
  TITLE     Ovarian tumor associated sequences
  JOURNAL   Patent: WO 0151513-A 1138 19-JUL-2001;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
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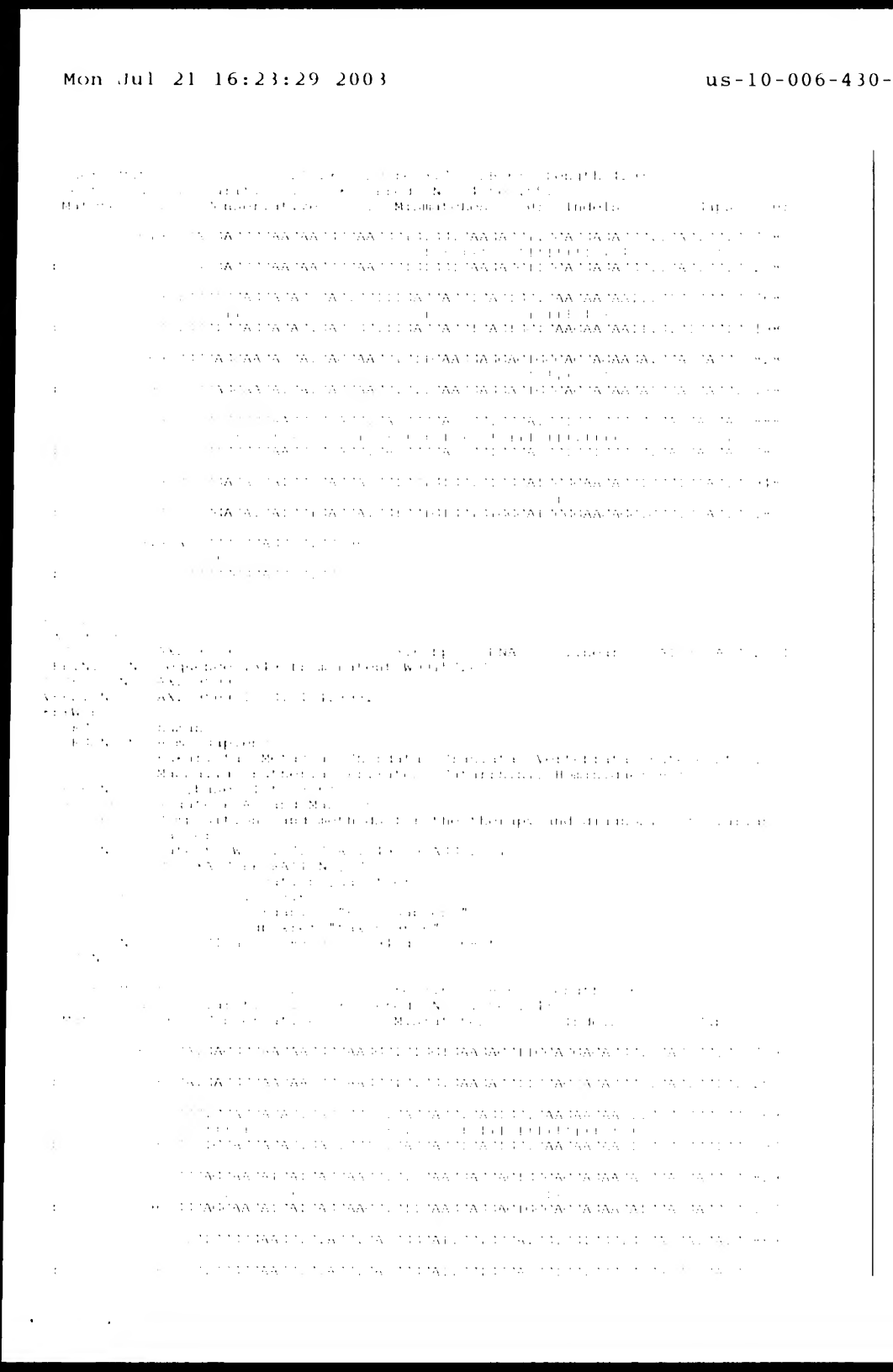

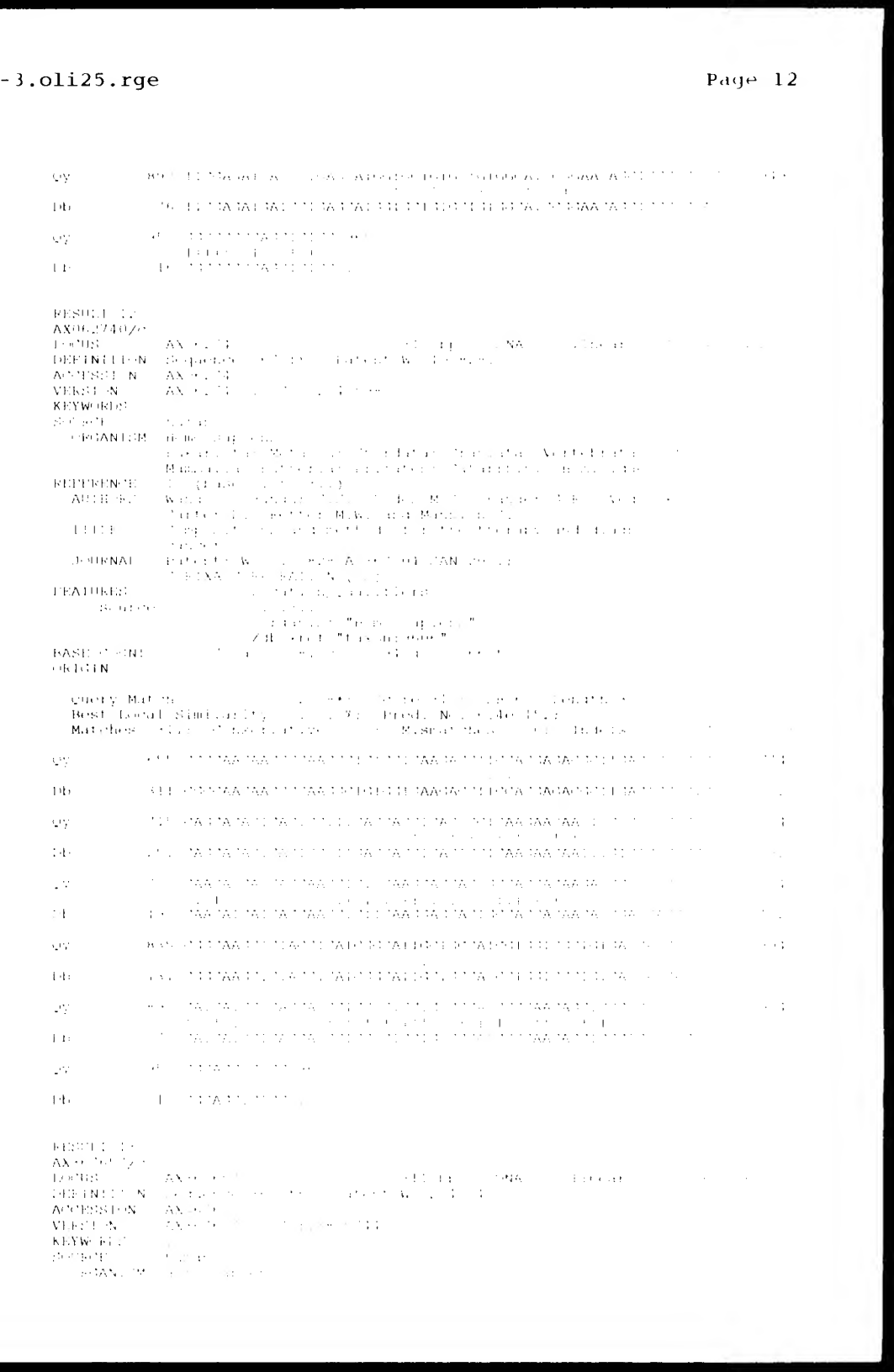

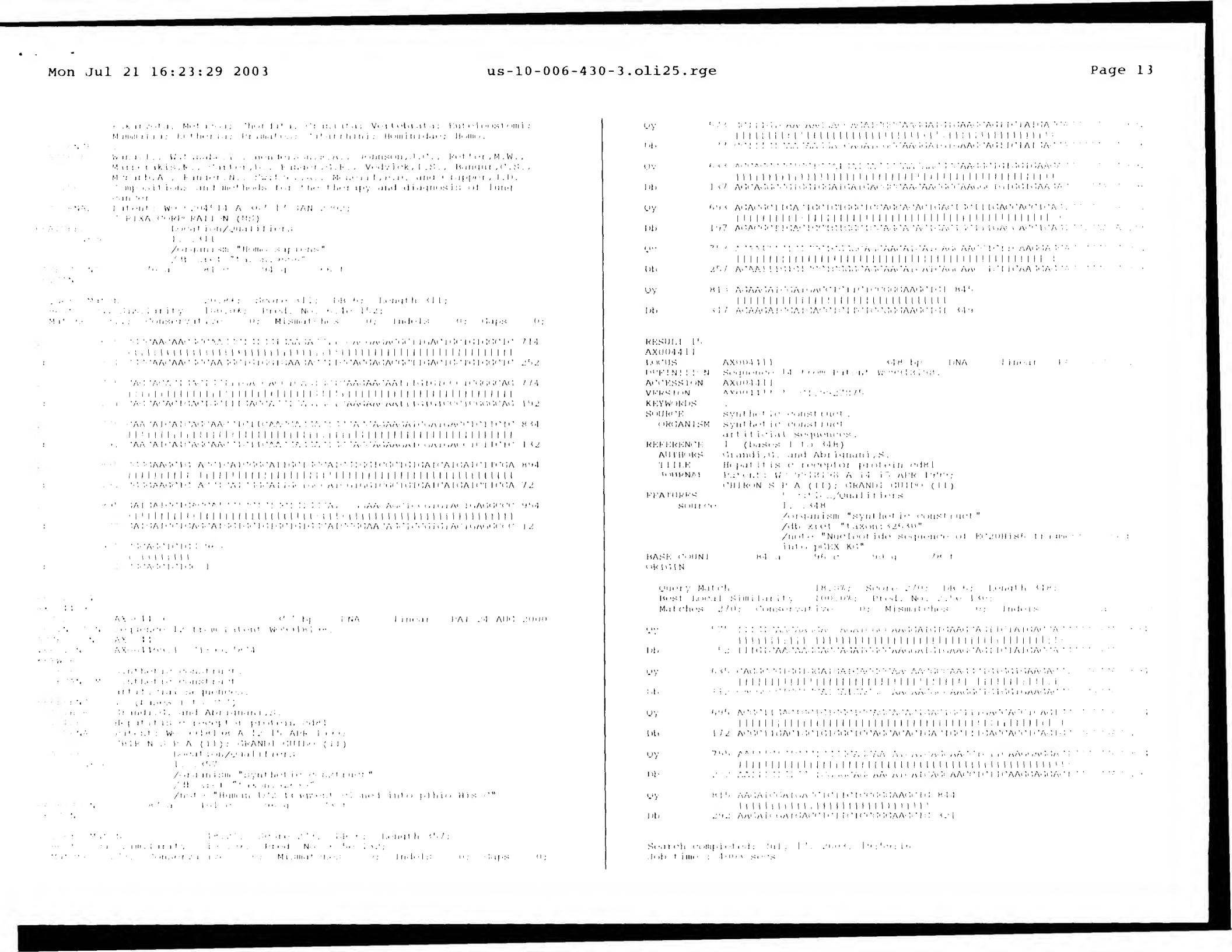

[illegible] nucleic search, using sw model

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(without alignments)
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SUMMARIES

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[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	AA[illegible]	Human colon cancer
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	AAH[illegible]	Human secreted pro
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	ABN[illegible]	Human [illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	AAH[illegible]	Human ovarian tumo
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	AA[illegible]	Human ovarian [illegible]
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[illegible]	[illegible]	[illegible]	[illegible]	24	ABK[illegible]	cDNA encoding [illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	AAX[illegible]	DNA [illegible]
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16	171	11.4	[illegible]	22	AAS[illegible]	Human [illegible]
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c 26	[illegible]	[illegible]	[illegible]	24	ABN[illegible]	[illegible]
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c 31	[illegible]	[illegible]	[illegible]	24	AB[illegible]	[illegible]
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ALIGNMENTS

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XX
DT [illegible] MAY 2002 (first entry)
XX
DE Prostate cancer related [illegible]
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; [illegible]
KW stomach; liver; prostate; pancreas; [illegible]
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; [illegible]
KW gene; ds.
XX
OS Homo sapiens.
XX
PN [illegible]
XX
PD [illegible]
XX
PF [illegible] MAY [illegible]
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PR 05-JUN-2000; [illegible]
PR [illegible]
PR 18-SEP-2000; 2000US-[illegible]
PR 18-SEP-2000; [illegible]
PR [illegible]
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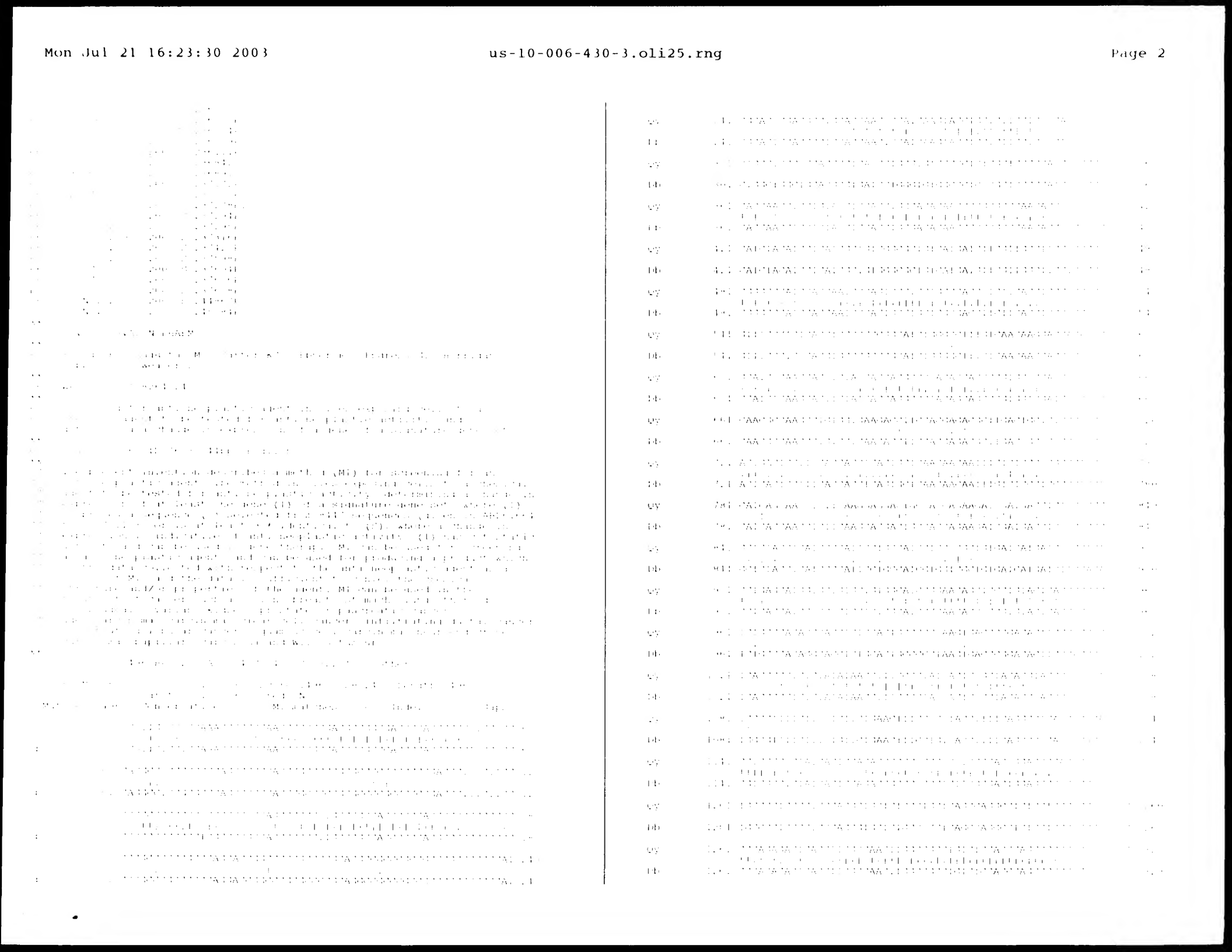

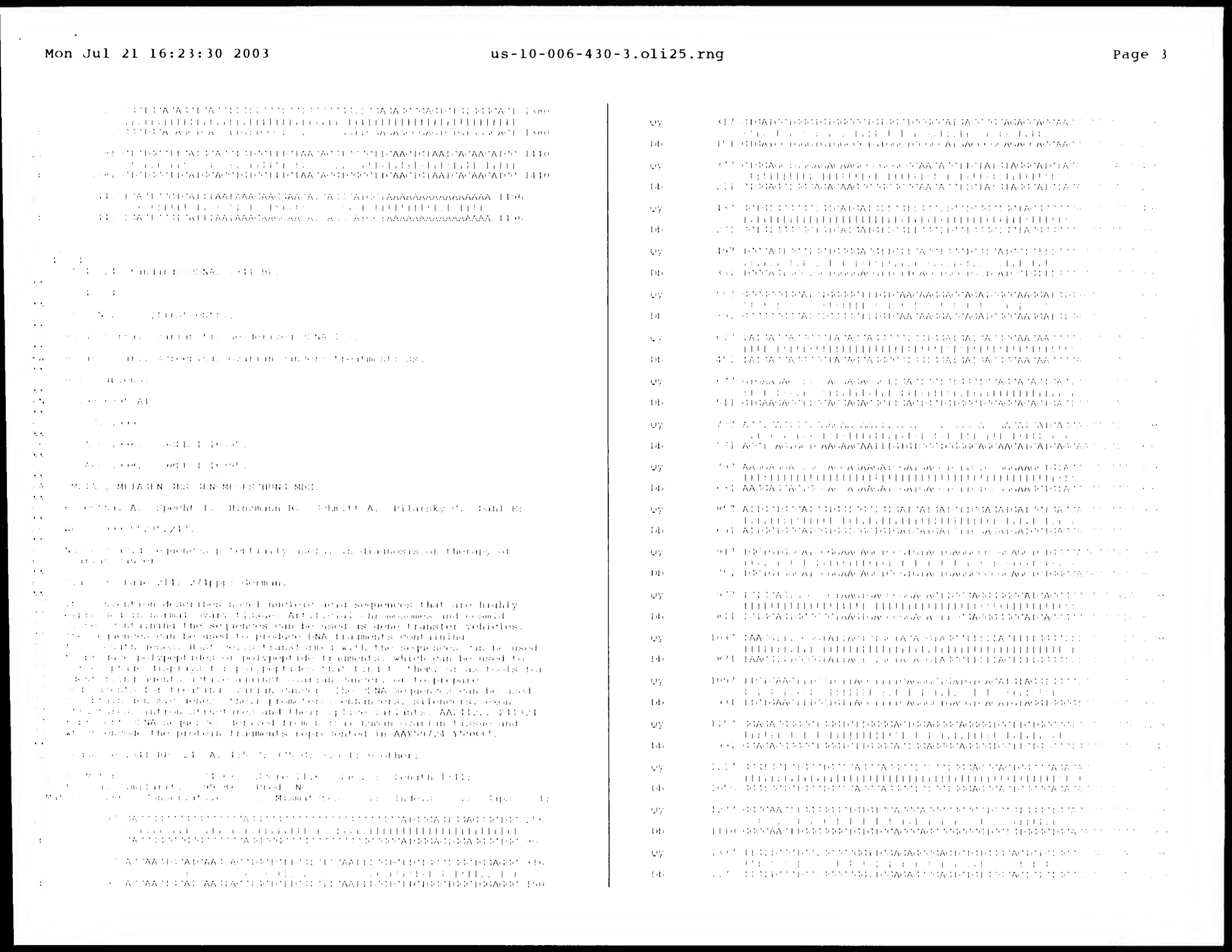

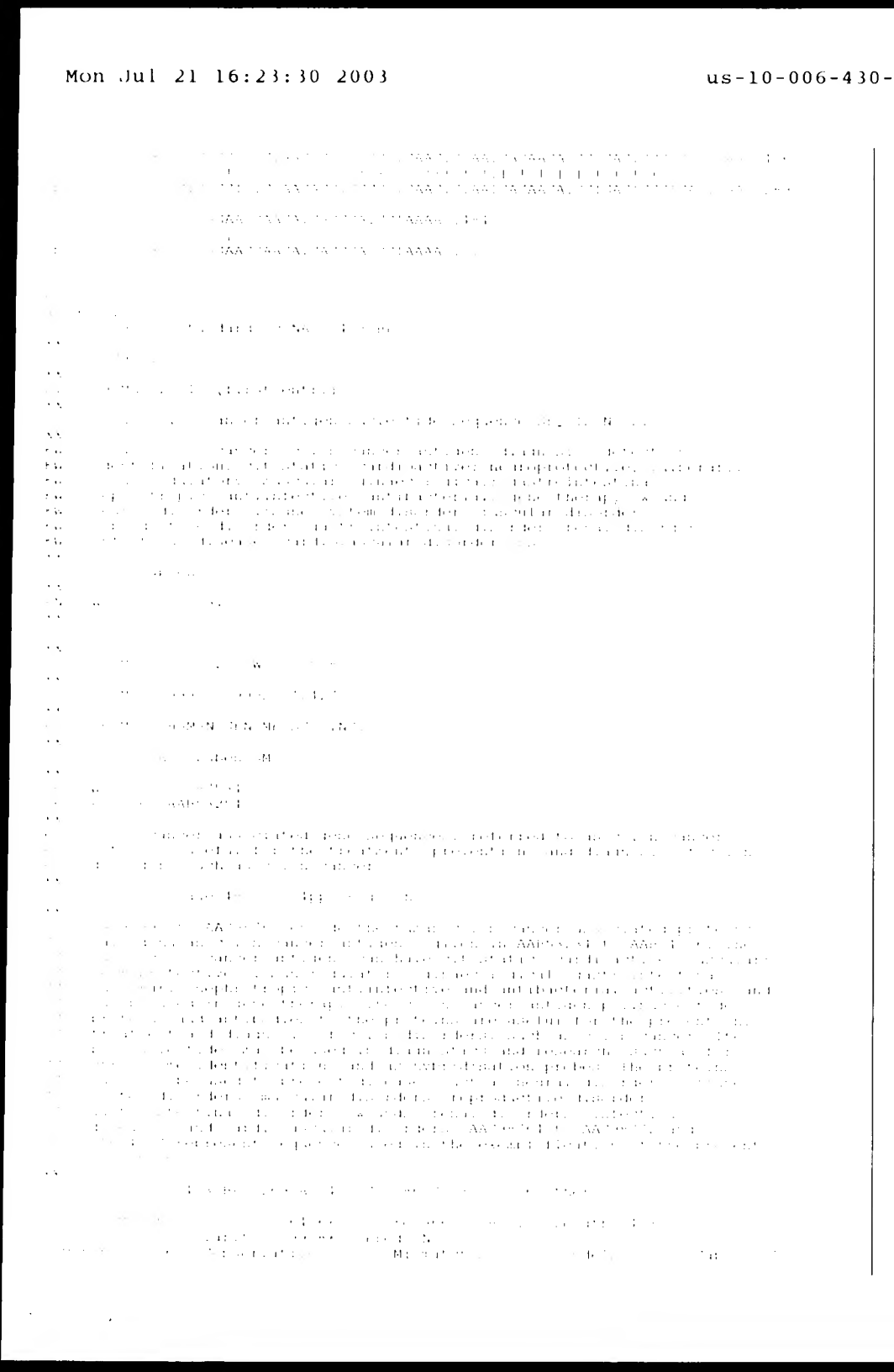

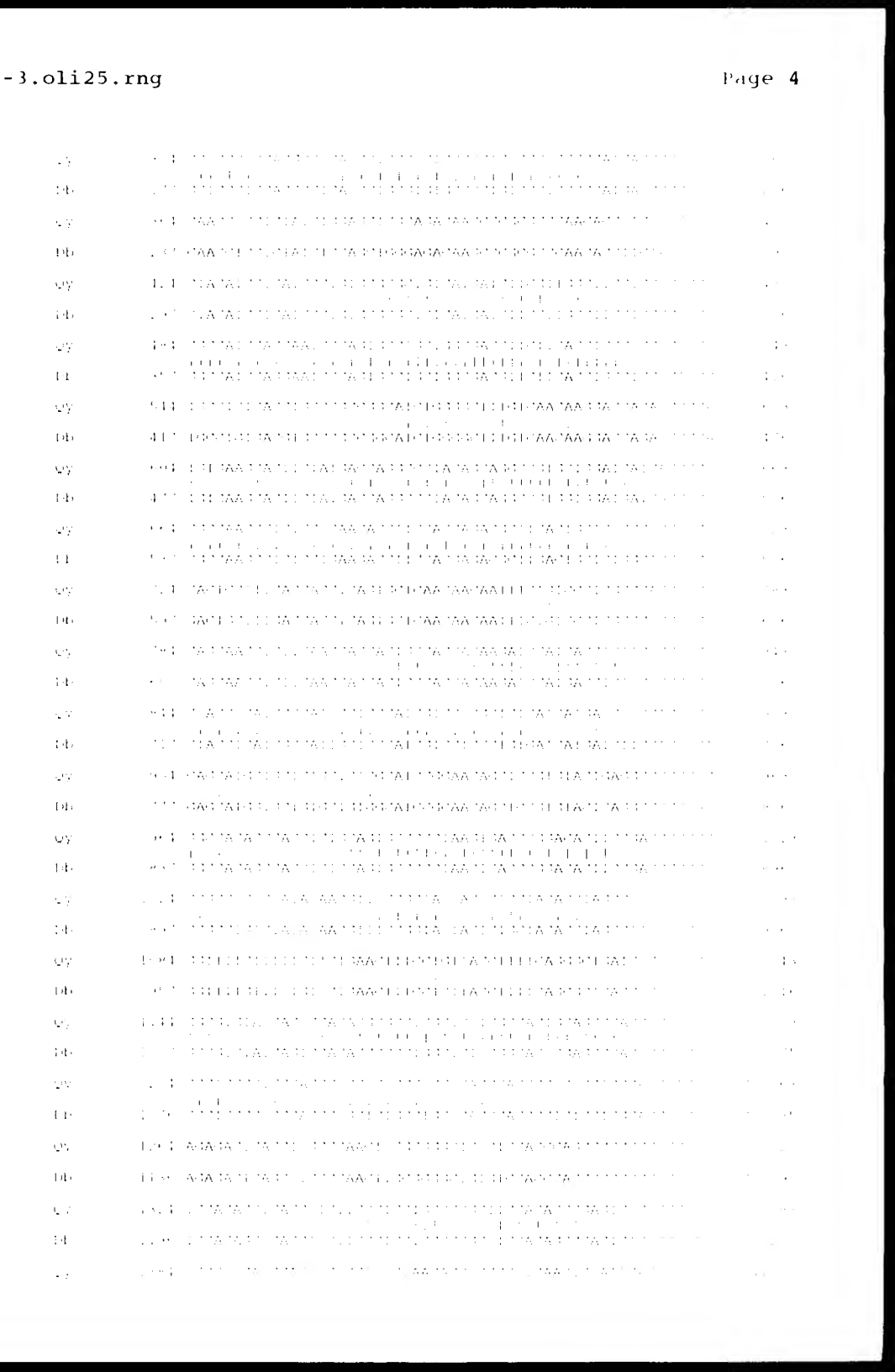

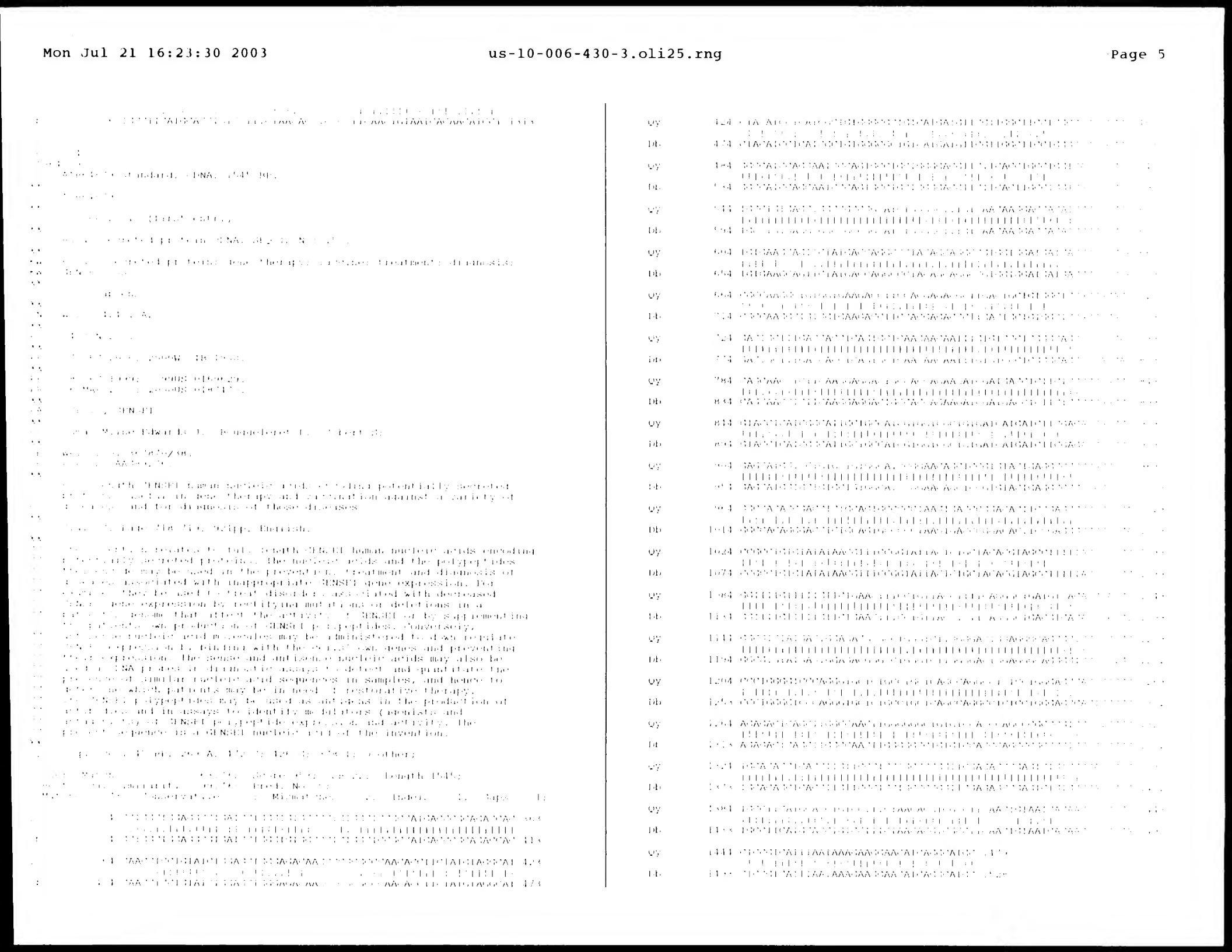

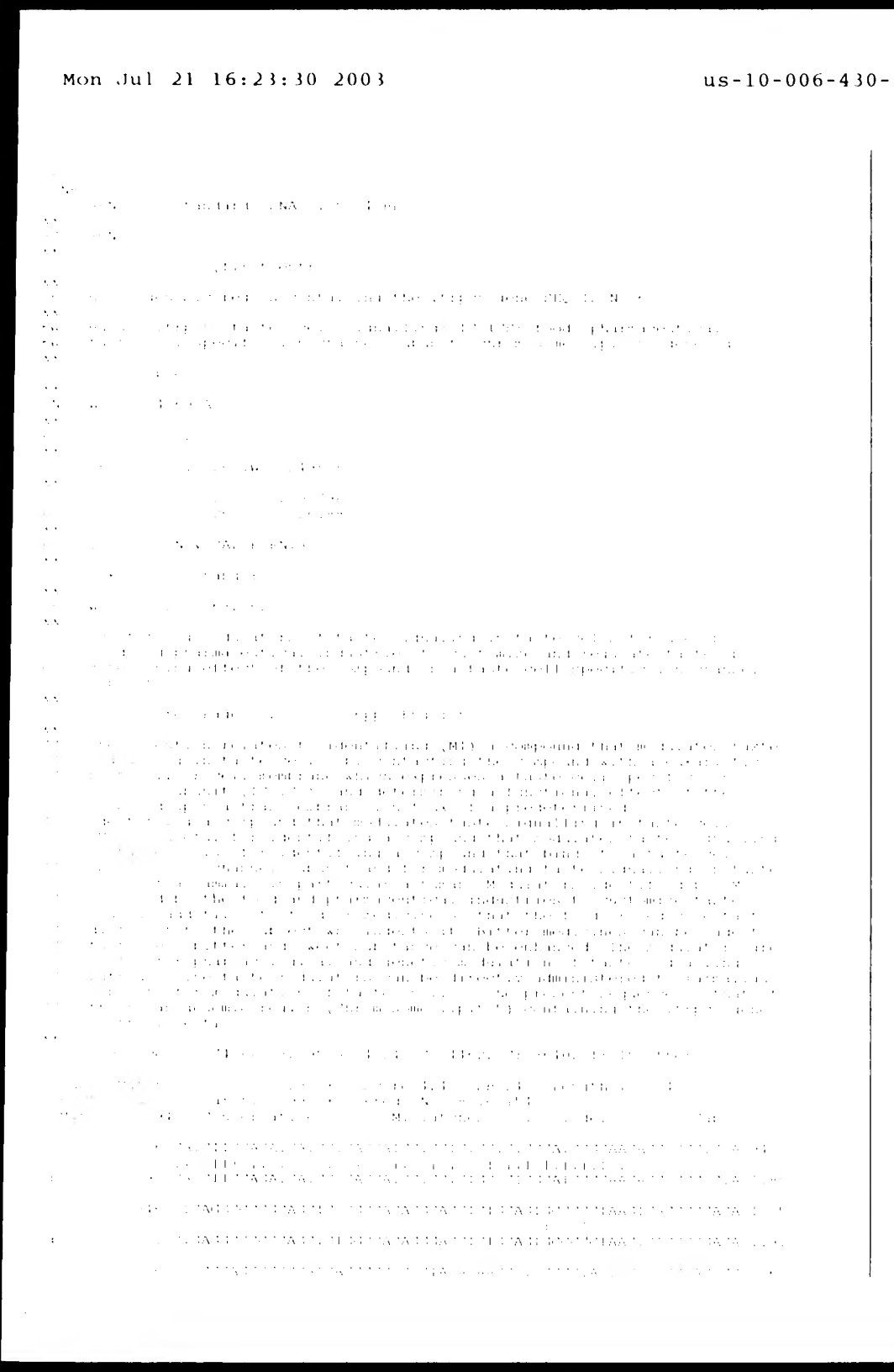

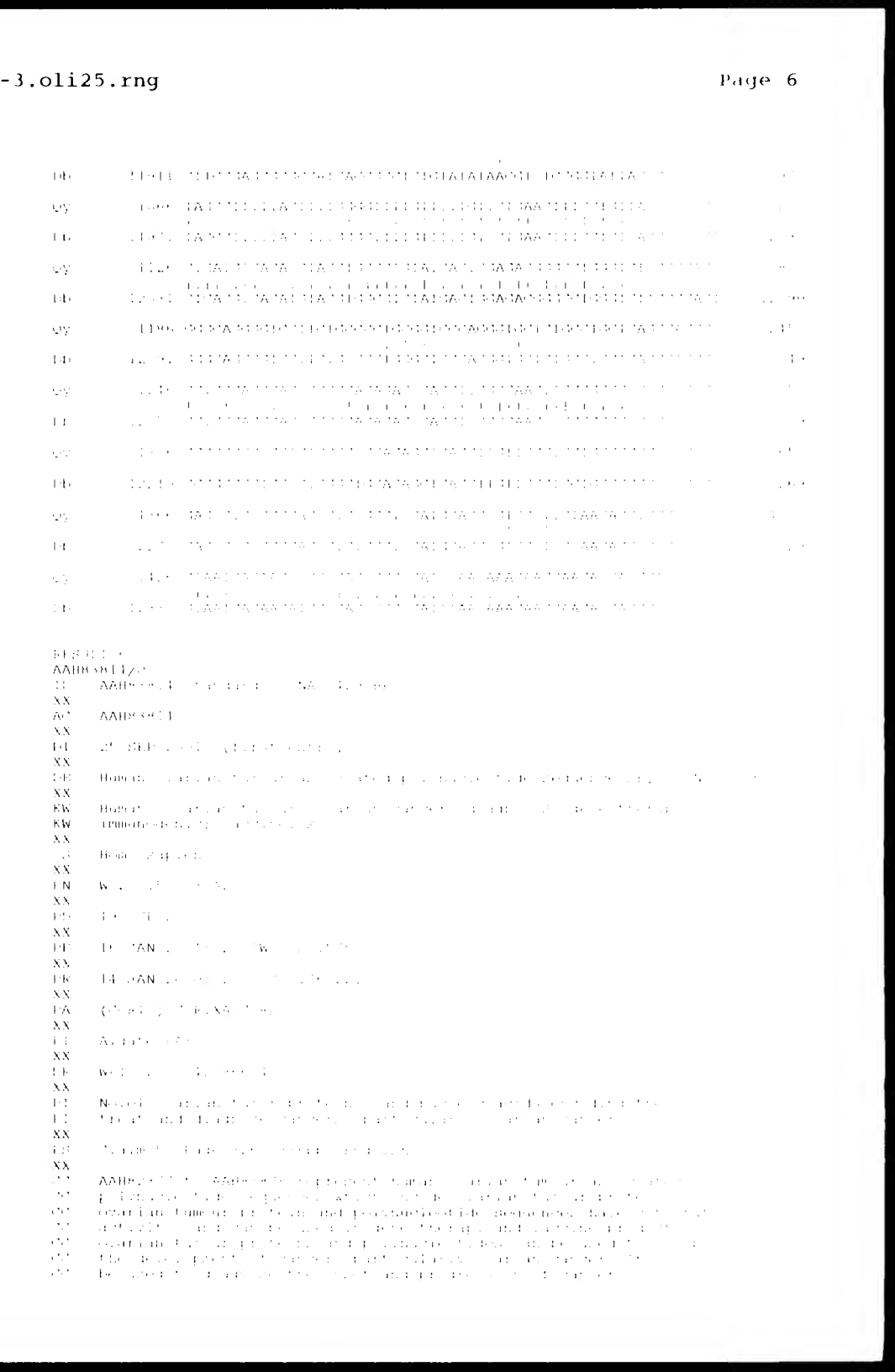

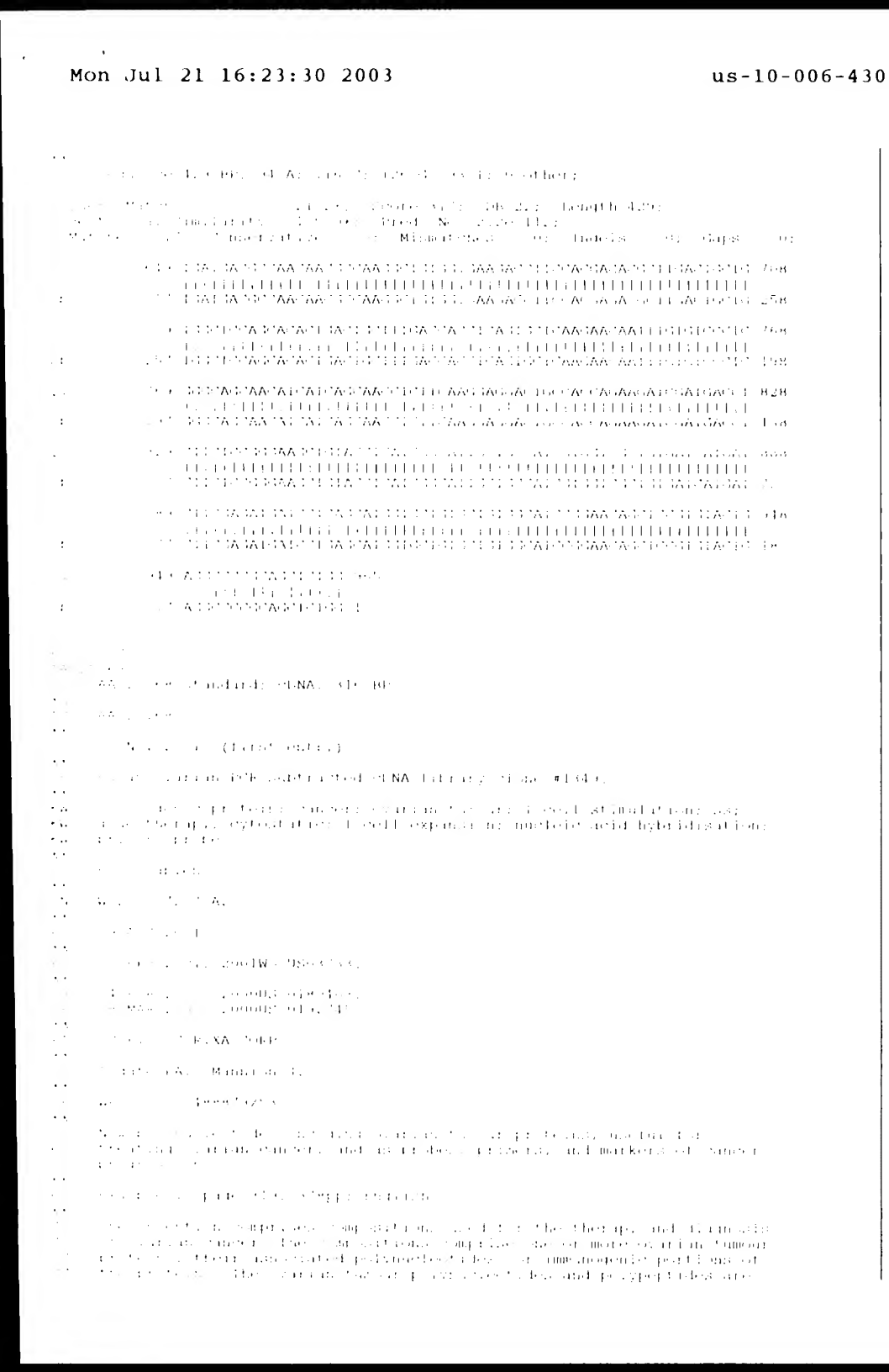

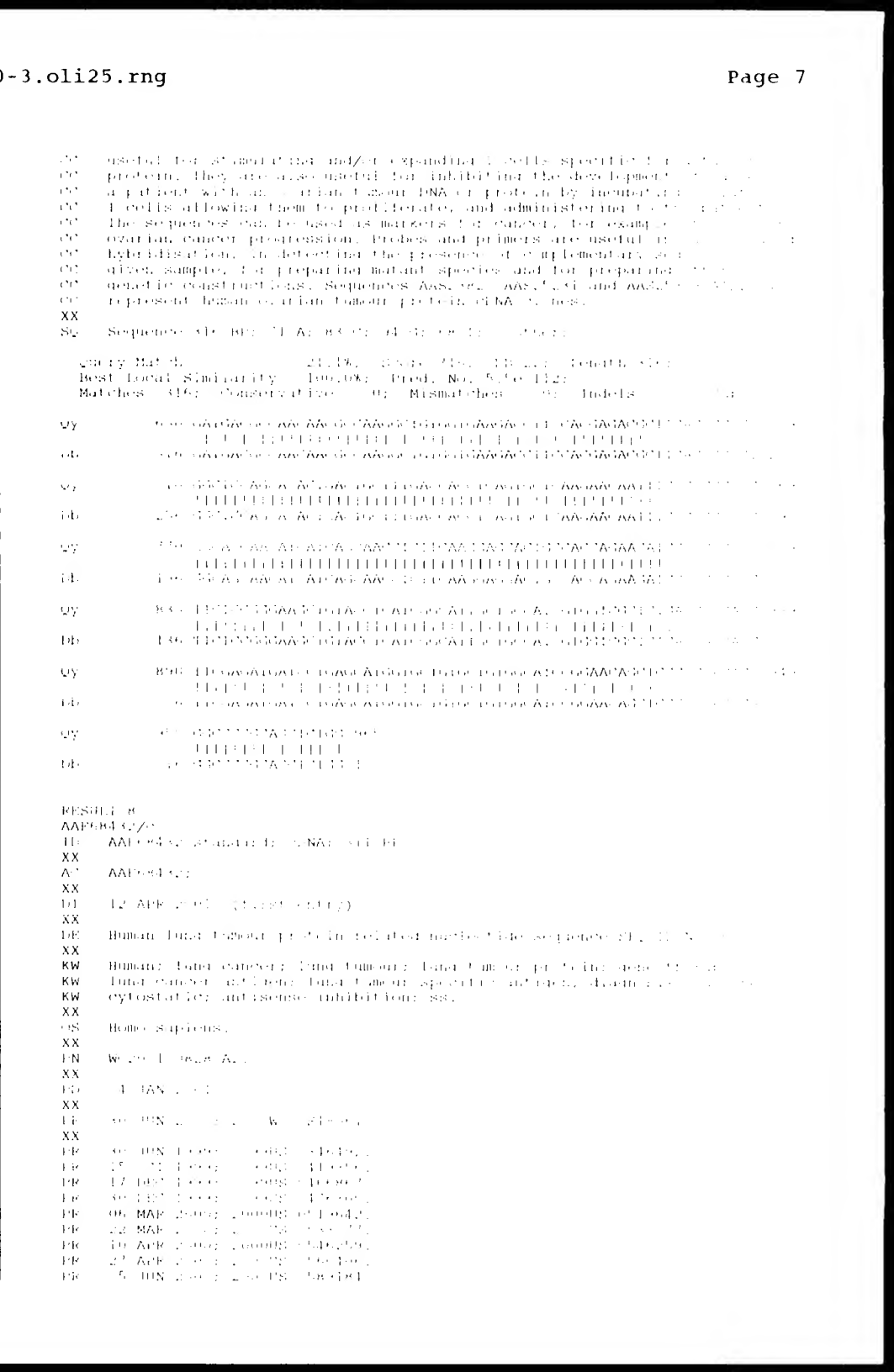

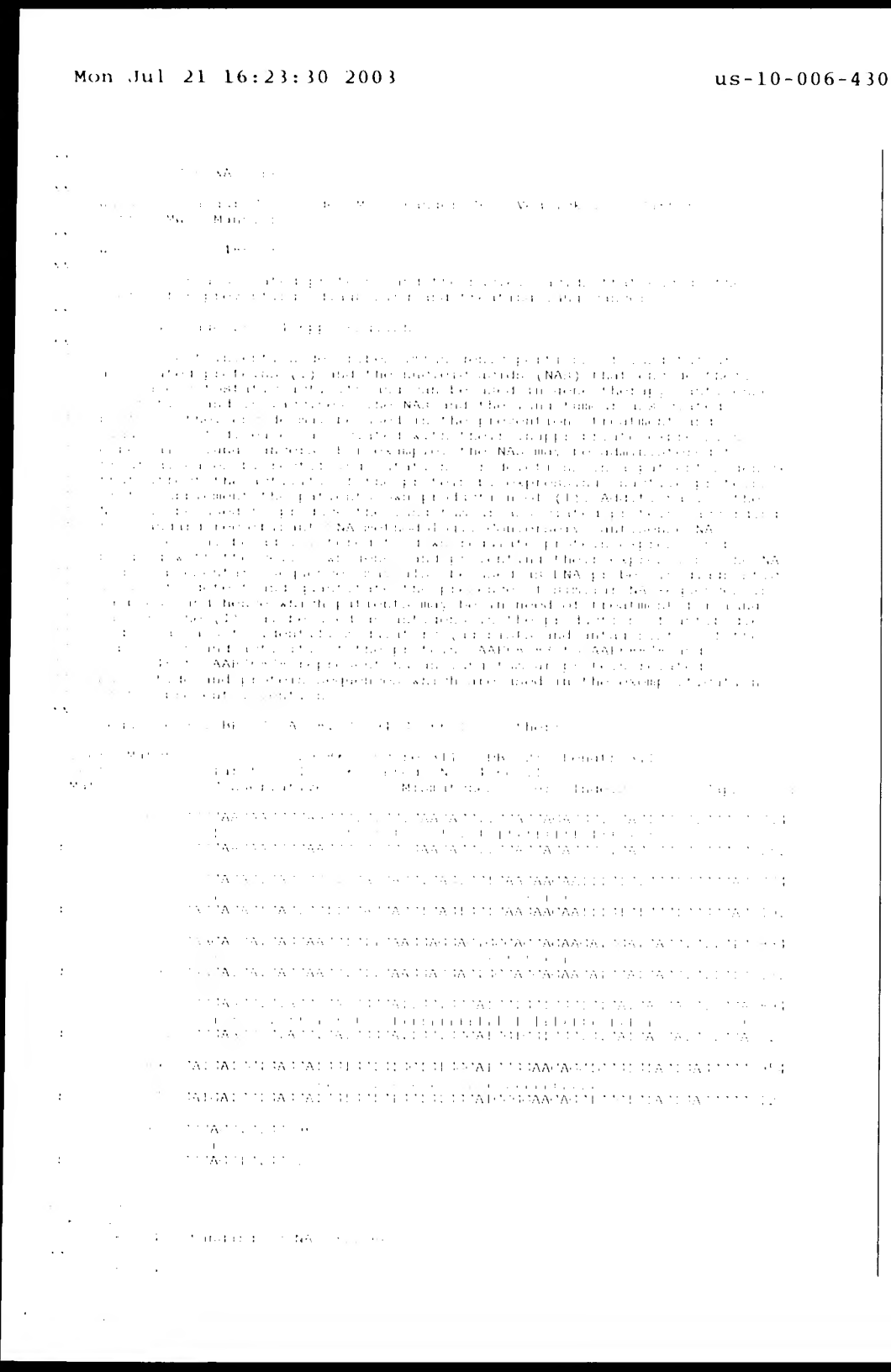

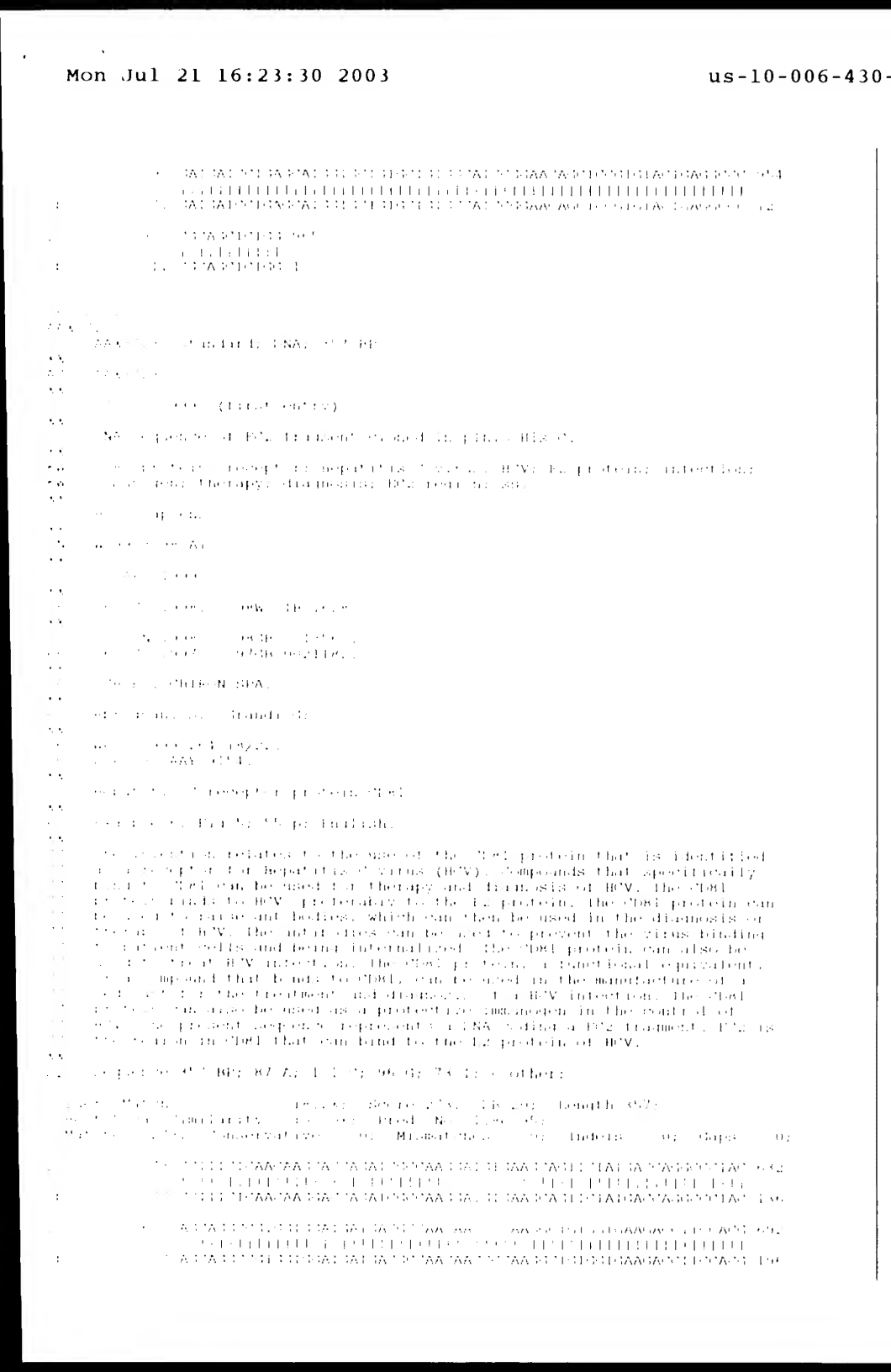

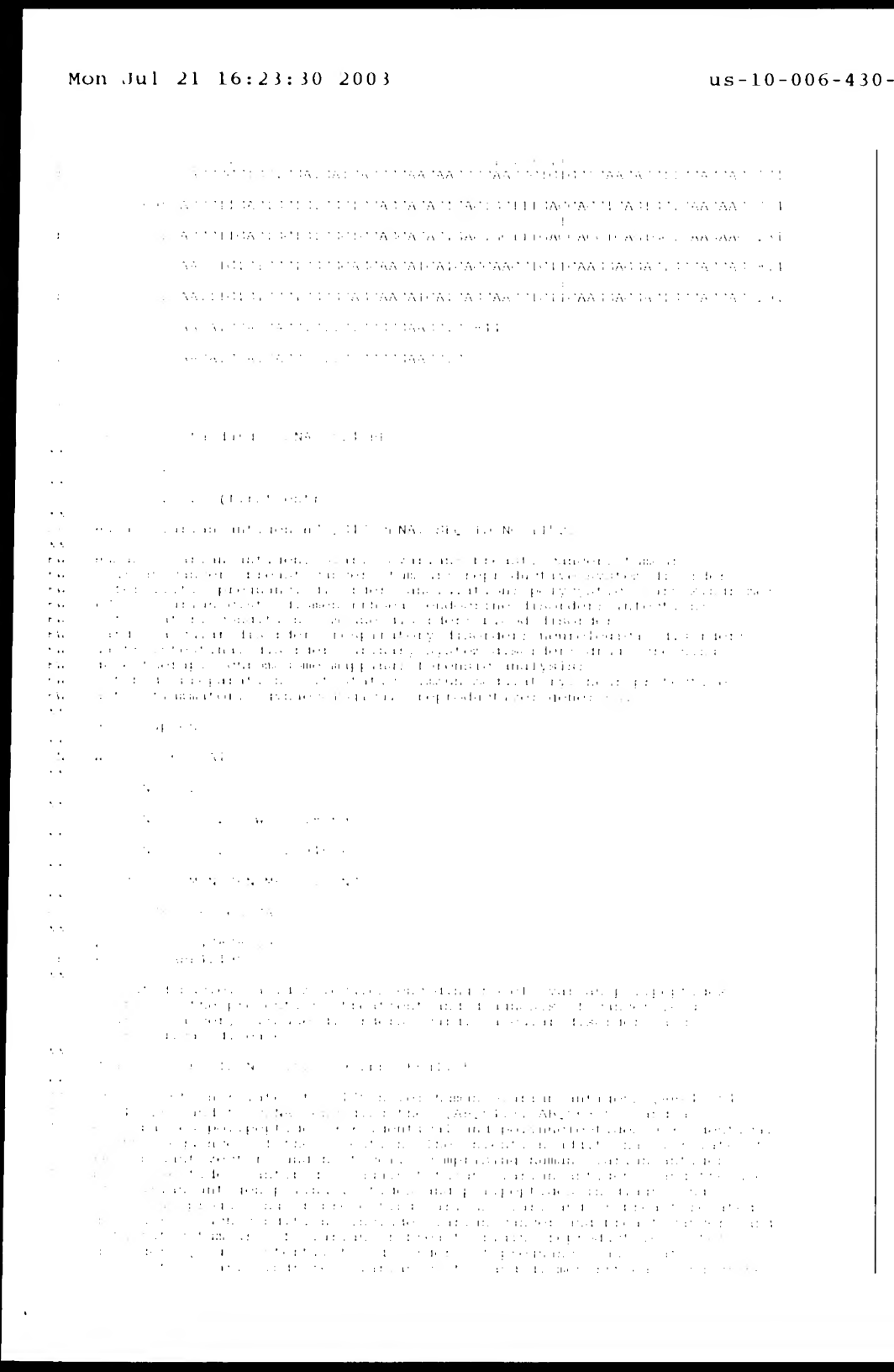

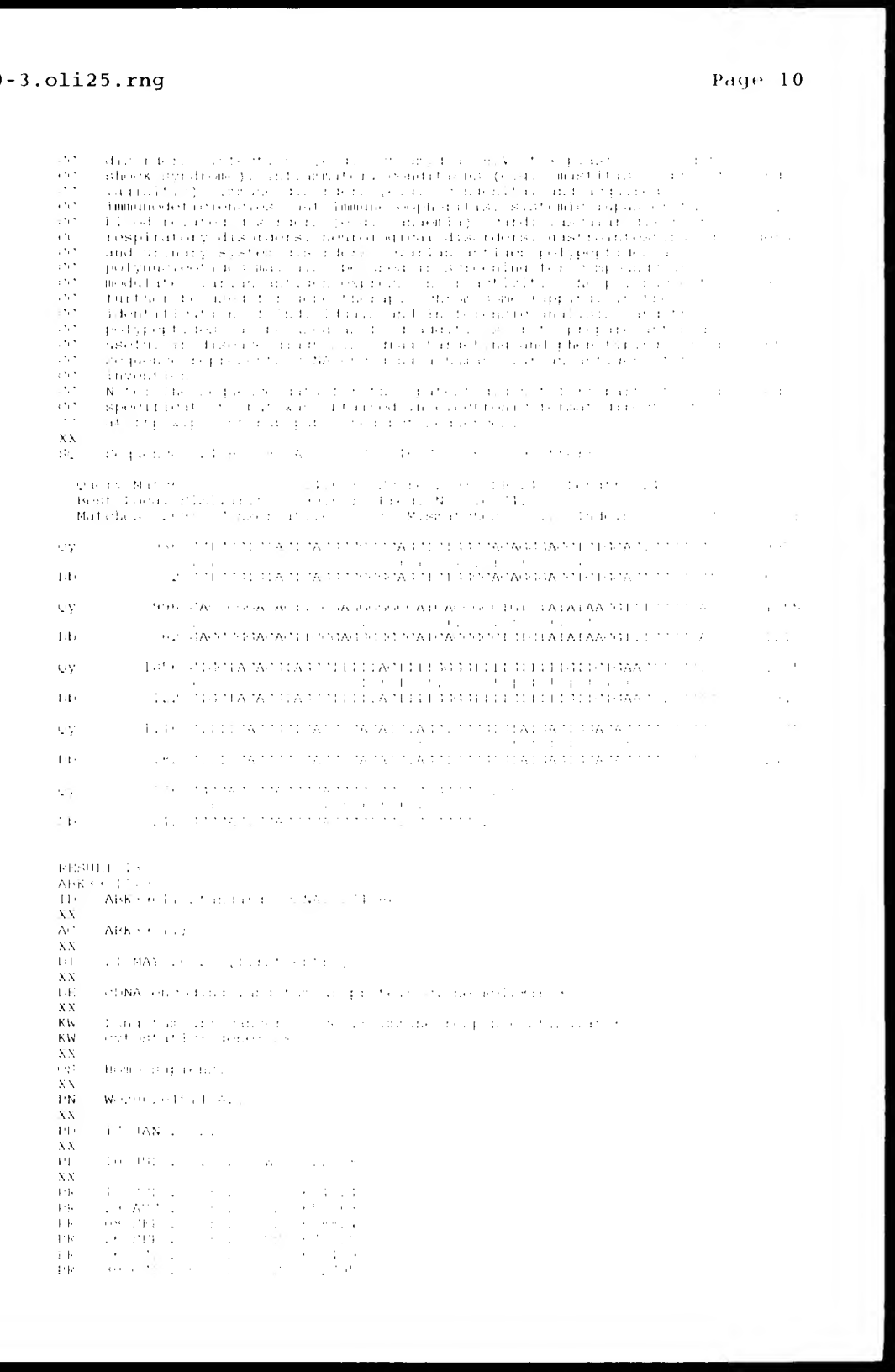

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PR [illegible] 2001; 2001US 0849626.
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PA (CORI-) CORIXA CORP.
XX
PI Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
PI Marmetakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS;
PI Menabb A, Wang A, Fanger N, Switzer A, Menerill PD, Clapper JD;
XX
DR WPI; 2002-164634/21.
XX
PT Novel polynucleotide encoding a lung tumour polypeptide useful for
PT stimulating and/or expanding T cells specific for a tumour protein
XX
PS Claim 1; SEQ ID No [illegible]; 223pp; English.
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CC The invention describes an isolated polynucleotide and polypeptide
CC useful for stimulating and/or expanding T cells specific for a tumour
CC protein for determining the presence of a cancer in a patient. A
CC composition containing the polynucleotide and/or polypeptide is useful
CC for treating a lung cancer in a patient. The polypeptide is useful for
CC removing tumour cells from a biological sample. The polynucleotide is
CC also useful as probe or primer to detect the level of mRNA encoding a
CC tumour protein. This sequence encodes a lung tumour associated protein
CC or protein fragment, described in the method of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
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PF [illegible] 2001WO-[illegible]

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PR 08-SEP-2000; 2000US 0658824.
PR 26-SEP-2000; 2000US 0671325.
PR 06-OCT-2000; 2000US 0677419.
PR 30-OCT-2000; 2000US 0702705.
PR 13-DEC-2000; 2000US 0736457.
PR 03-MAY-2001; 2001US 0849626.
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PI Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
PI Marmetakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS;
PI Menabb A, Wang A, Fanger N, Switzer A, Menerill PD, Clapper [illegible]
XX
DR WPI; 2002-164634/21.
XX
PT Novel polynucleotide encoding a lung tumour polypeptide useful for
PT stimulating and/or expanding T cells specific for a tumour protein
XX
PS Claim 1; SEQ ID No 1024; 223pp; English.
XX
CC The invention describes an isolated polynucleotide and polypeptide
CC useful for stimulating and/or expanding T cells specific for a tumour
CC protein for determining the presence of a cancer in a patient. A
CC composition containing the polynucleotide and/or polypeptide is useful
CC for treating a lung cancer in a patient. The polypeptide is useful for
CC removing tumour cells from a biological sample. The polynucleotide is
CC also useful as probe or primer to detect the level of mRNA encoding a
CC tumour protein. This sequence encodes a lung tumour associated protein
CC or protein fragment, described in the method of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
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XX
DT 28-JUN-1996 (first entry)
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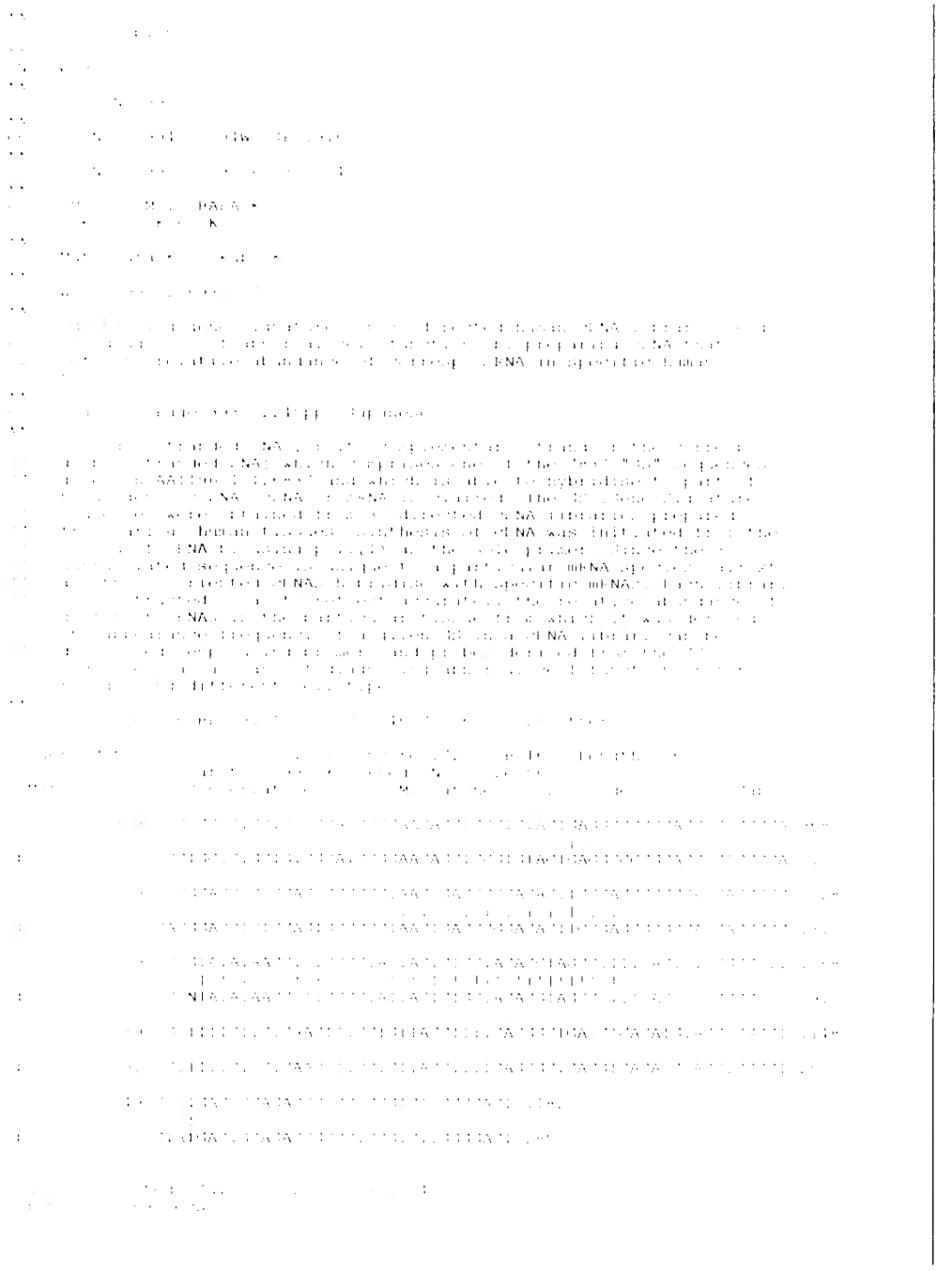
KW human; cloning; mapping; non biased library; diagnosis; [illegible]
KW cell typing; abnormal cell function; ss.



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Gapop 60.0 , Gapext 60.0

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Word size: 26

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	688	46.0	719	13	BI194523	[illegible]
9	688	46.0	913	14	BQ952334	[illegible]
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11	685	45.8	1116	14	BM799855	[illegible]
12	684	45.7	879	14	BQ677674	[illegible]
13	683	45.7	717	10	BE262461	[illegible]
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15	672	44.9	869	14	BQ218777	[illegible]
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17	669	44.7	973	9	AL529815	[illegible]
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23	642	42.9	797	13	BM051394	[illegible]
24	642	42.9	1059	14	BM915179	[illegible]
25	632	42.2	851	12	BG697401	[illegible]
26	632	42.2	931	14	BQ678654	[illegible]
27	625	41.8	902	14	BQ897712	[illegible]
28	614	41.0	929	9	AL541229	[illegible]
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ALIGNMENTS

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ACCESSION   BM920185
VERSION     BM920185.1  GI:19330564
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E[illegible]
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; H[illegible]
REFERENCE   1  (bases 1 to 1032)
  AUTHORS   NIH MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collect[illegible]
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs r mail.nih.gov
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             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium ([illegible]
             DNA Sequencing by: Agencourt Bioscience Corporation.
             Clone distribution: MGC clone distribution informat[illegible]
            found through the I.M.A.G.E. Consortium/LLNL at:
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            Plate: LLAM12780  row: h  column: 12
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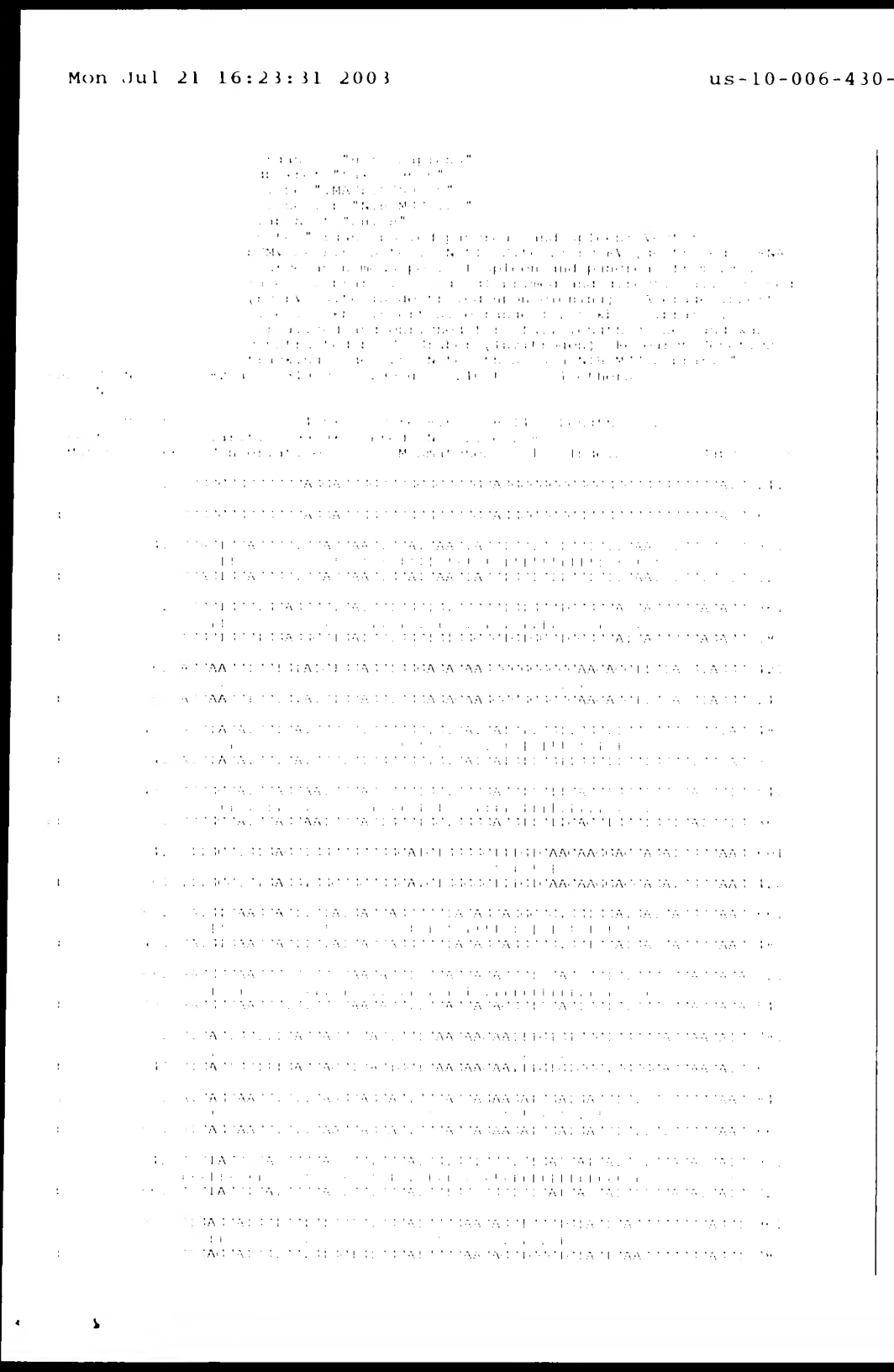

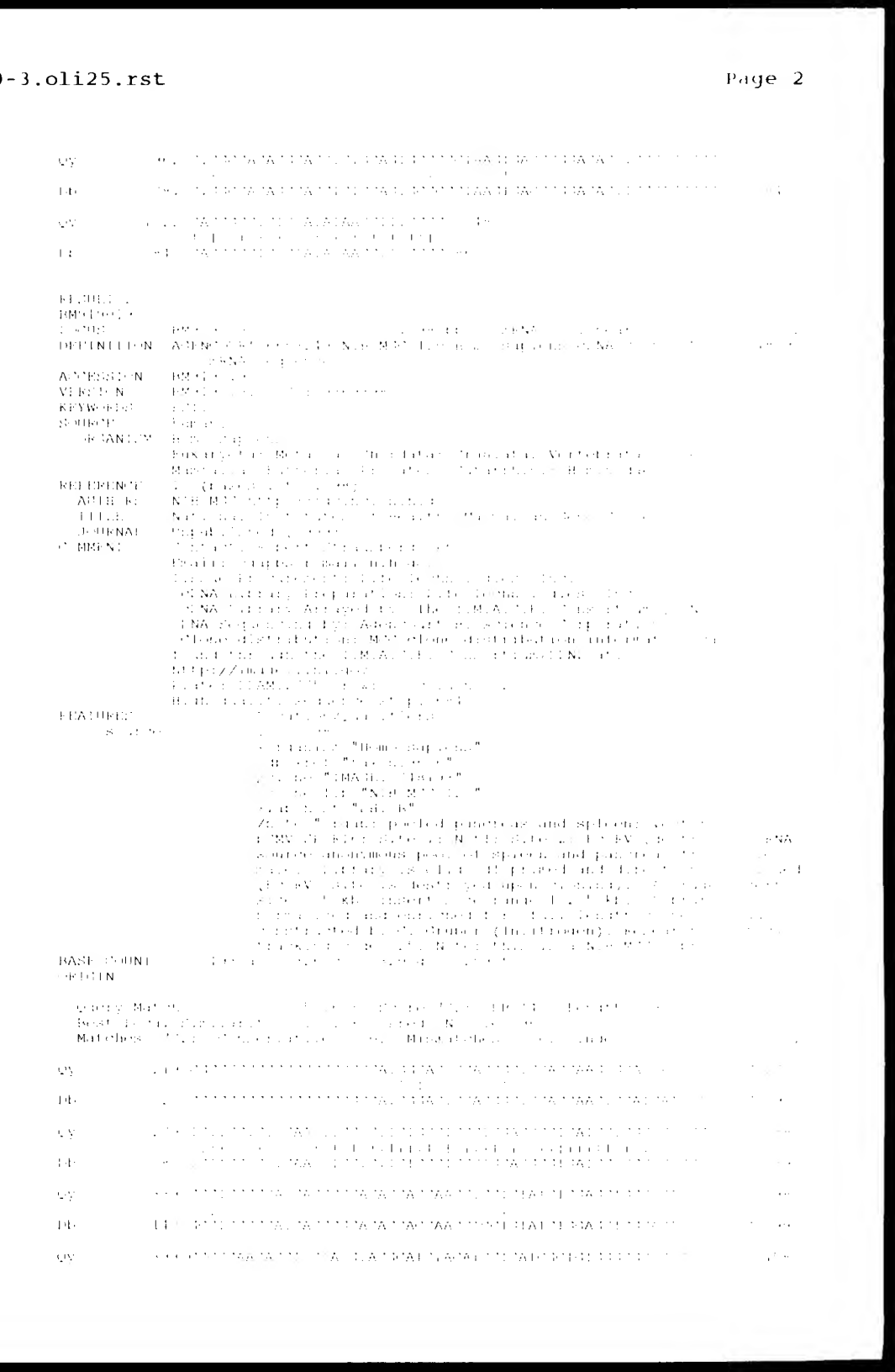

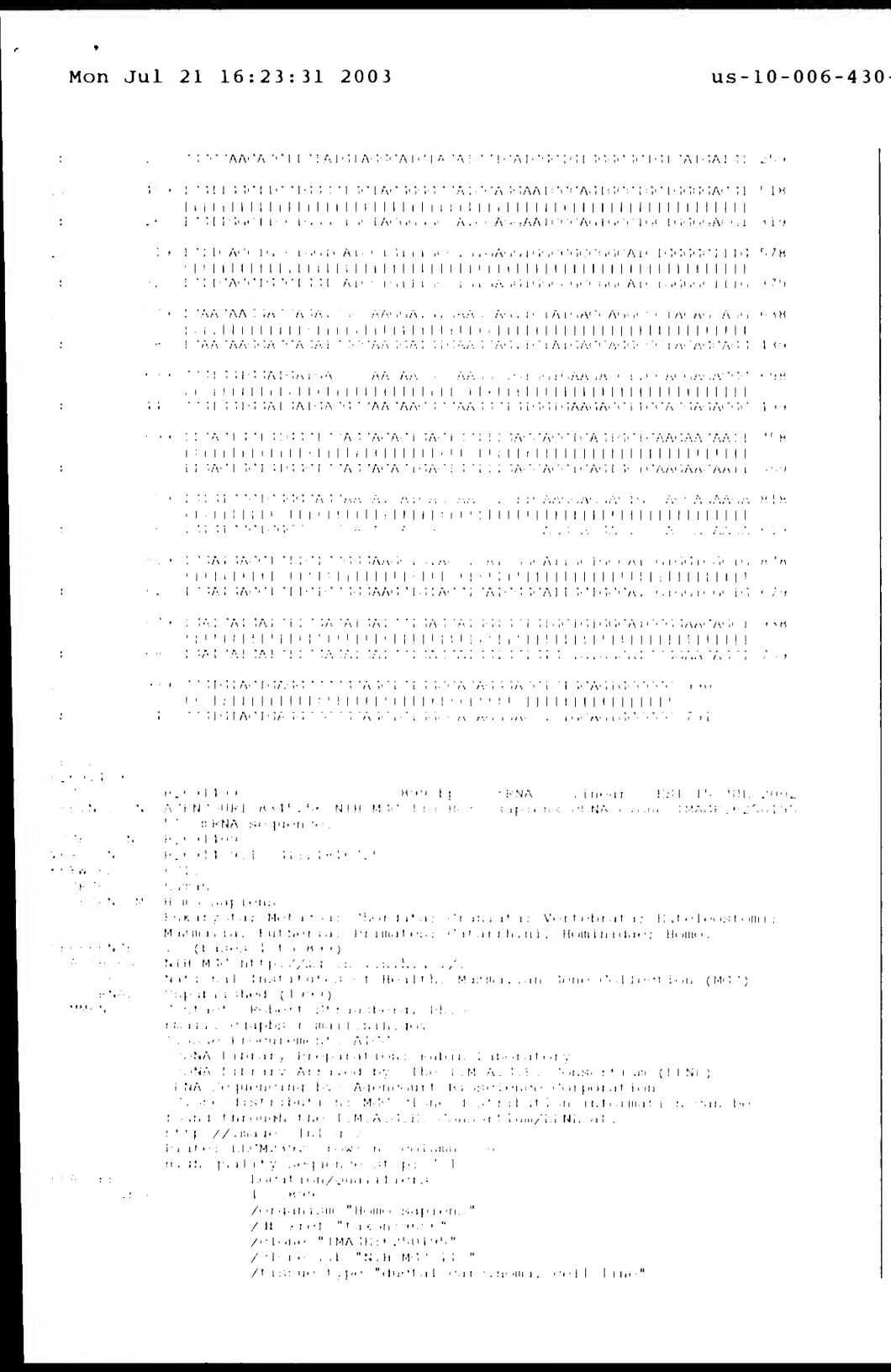

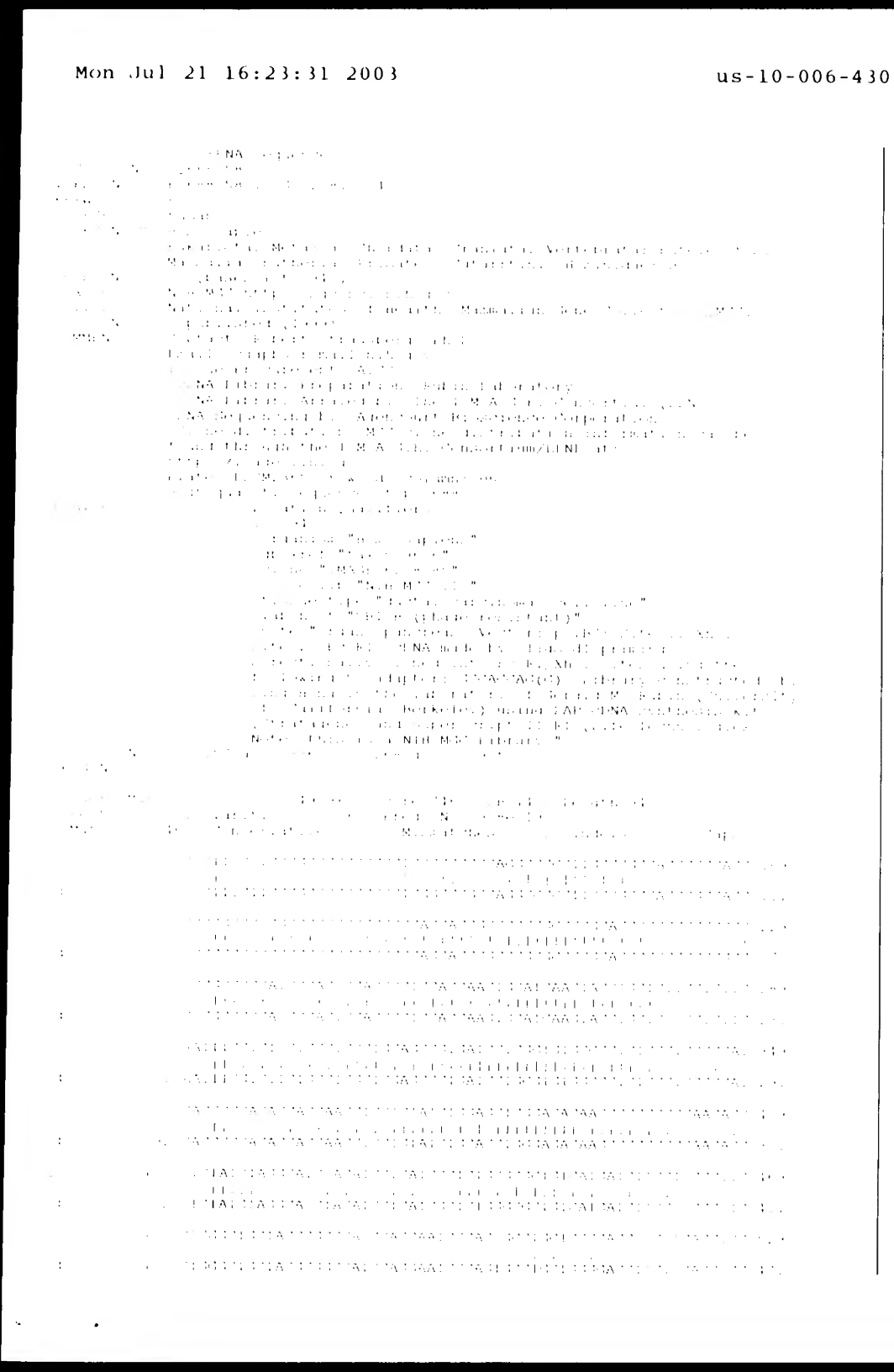

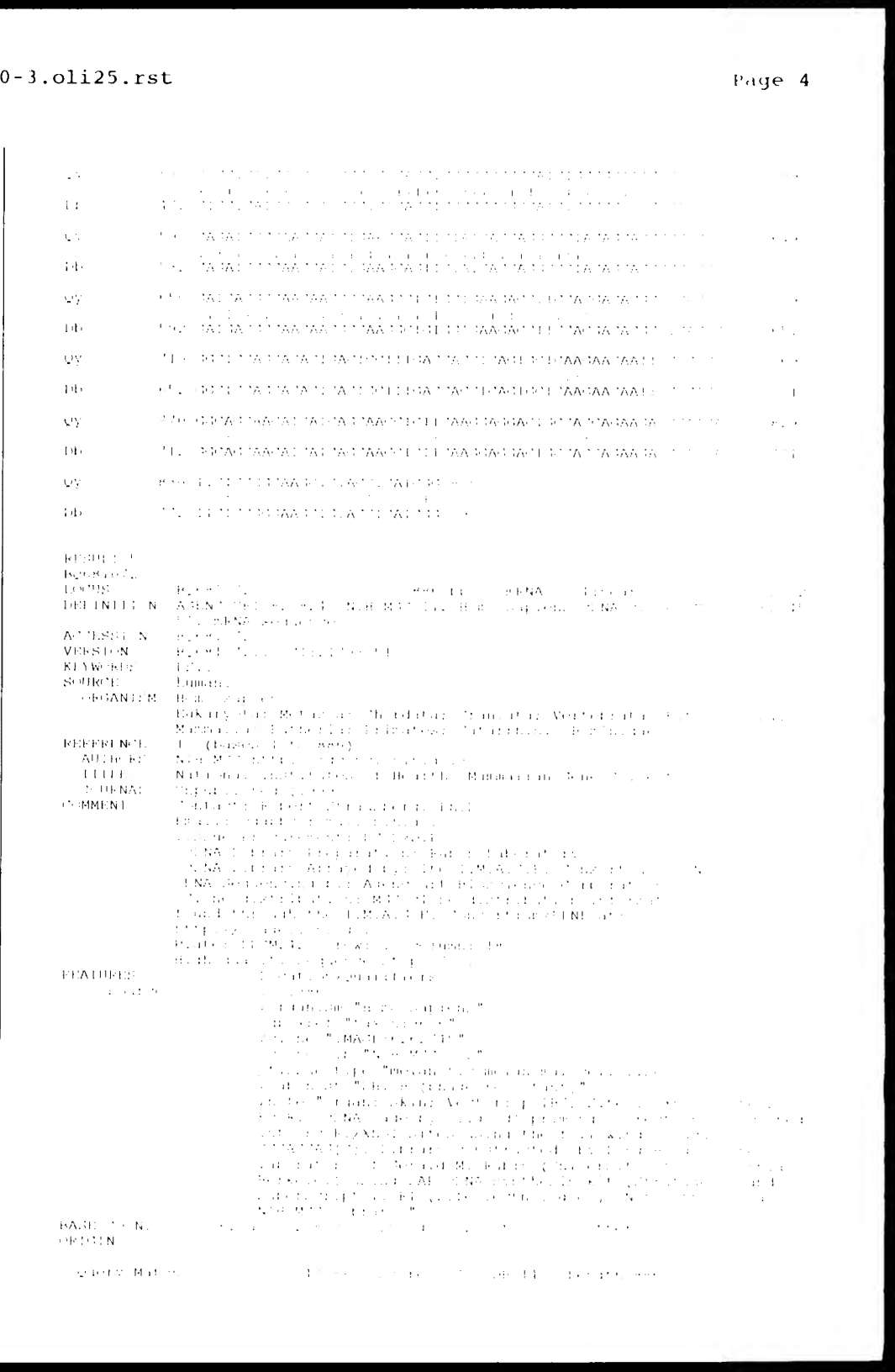

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Db        181 [illegible] 240

Qy        [illegible] 678
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Db        301 [illegible] 360

Qy        [illegible] 798
Db        361 [illegible] 420

Qy        [illegible] 858
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Qy        [illegible] 978
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[illegible]
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ACCESSION   [illegible]
VERSION     [illegible]  GI:[illegible]
KEYWORDS    EST.
SOURCE      human
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 764)
  AUTHORS   NIH MGC [illegible]
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information [illegible]
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM[illegible] row: [illegible] column: 11
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                     and male age 26 weeks. Library is oligo dT [illegible]
                     directionally cloned (EcoRV site is destroyed [illegible]
                     cloning). Average insert size 1.7 kb, insert [illegible]
                     0.7 - 3.5 kb. Library is normalized and enriched [illegible]
                     full length clones and was constructed by [illegible]
                     (Invitrogen). Research Genetics tracking [illegible]
                     This is a NIH MGC Library."
BASE COUNT      143 a    220 c    208 g    193 t
ORIGIN

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Db         61 [illegible]

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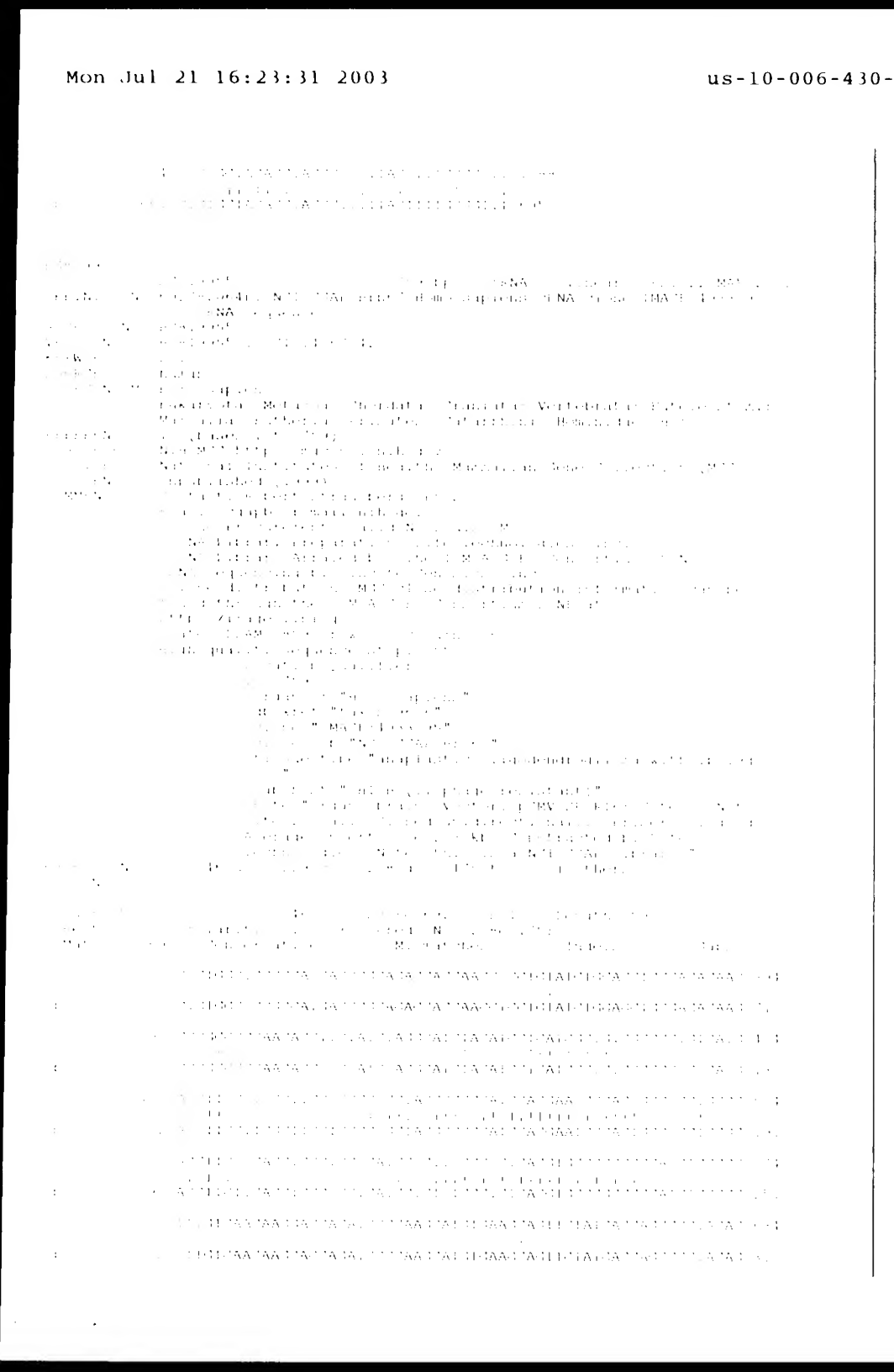

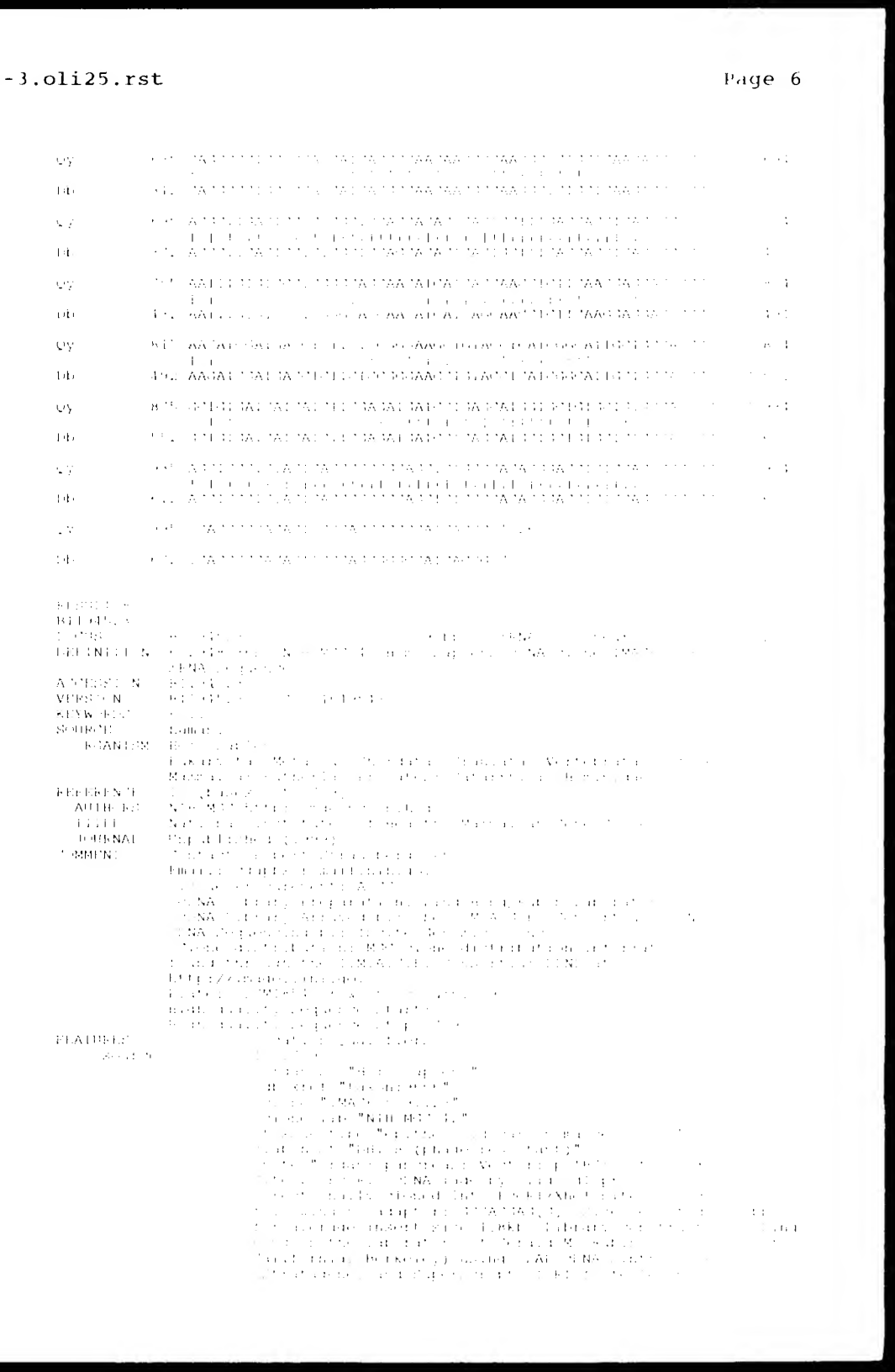

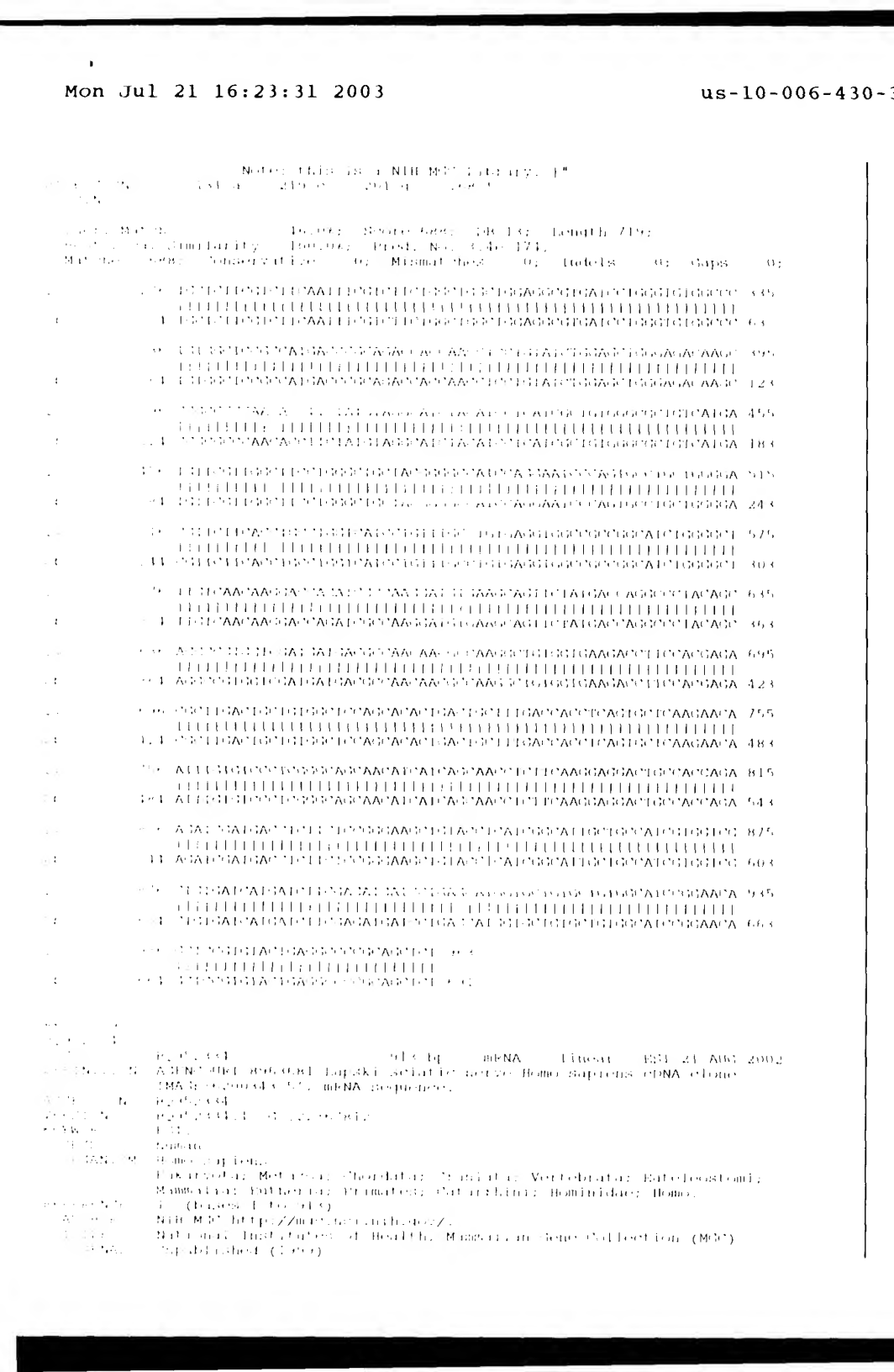

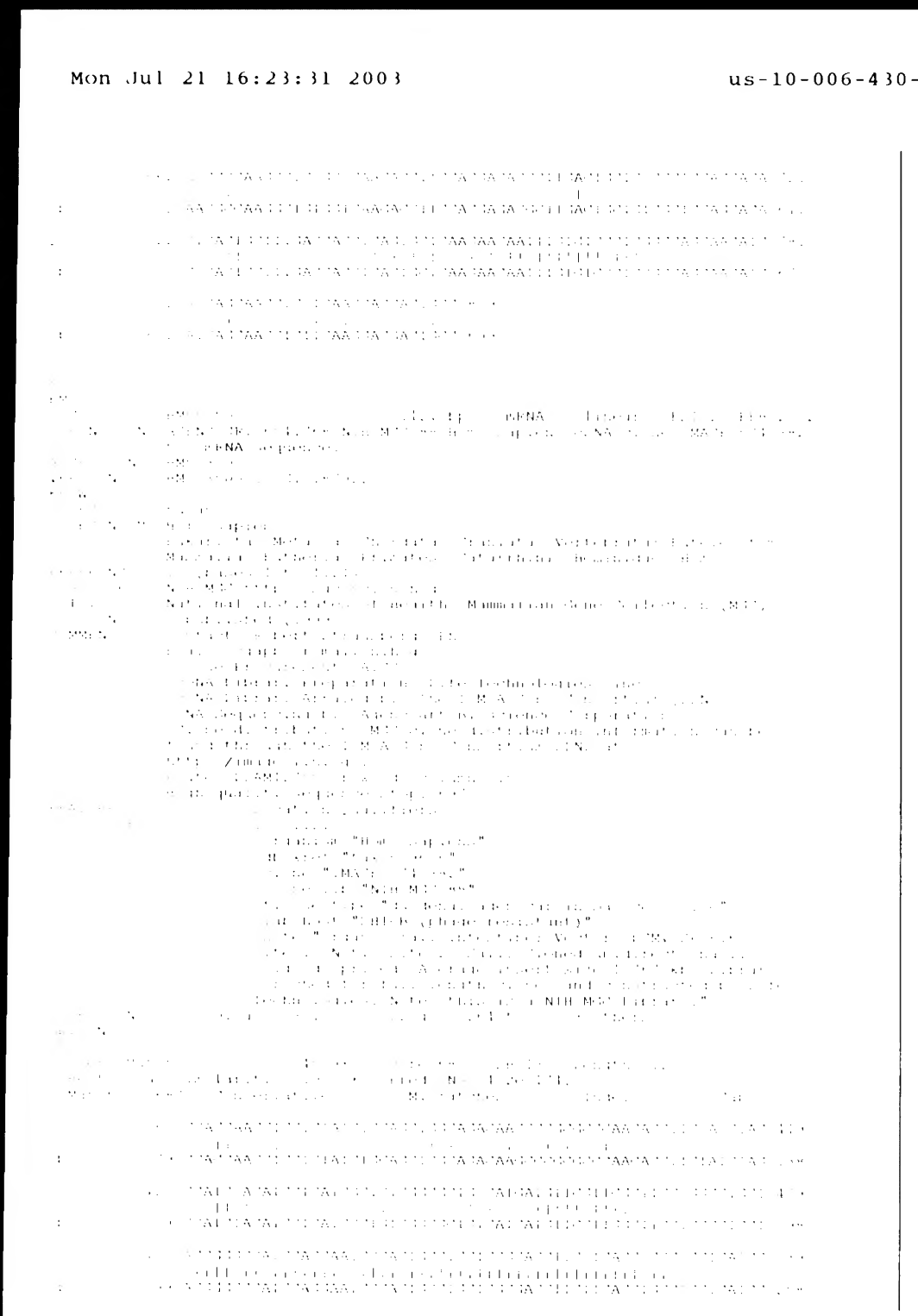

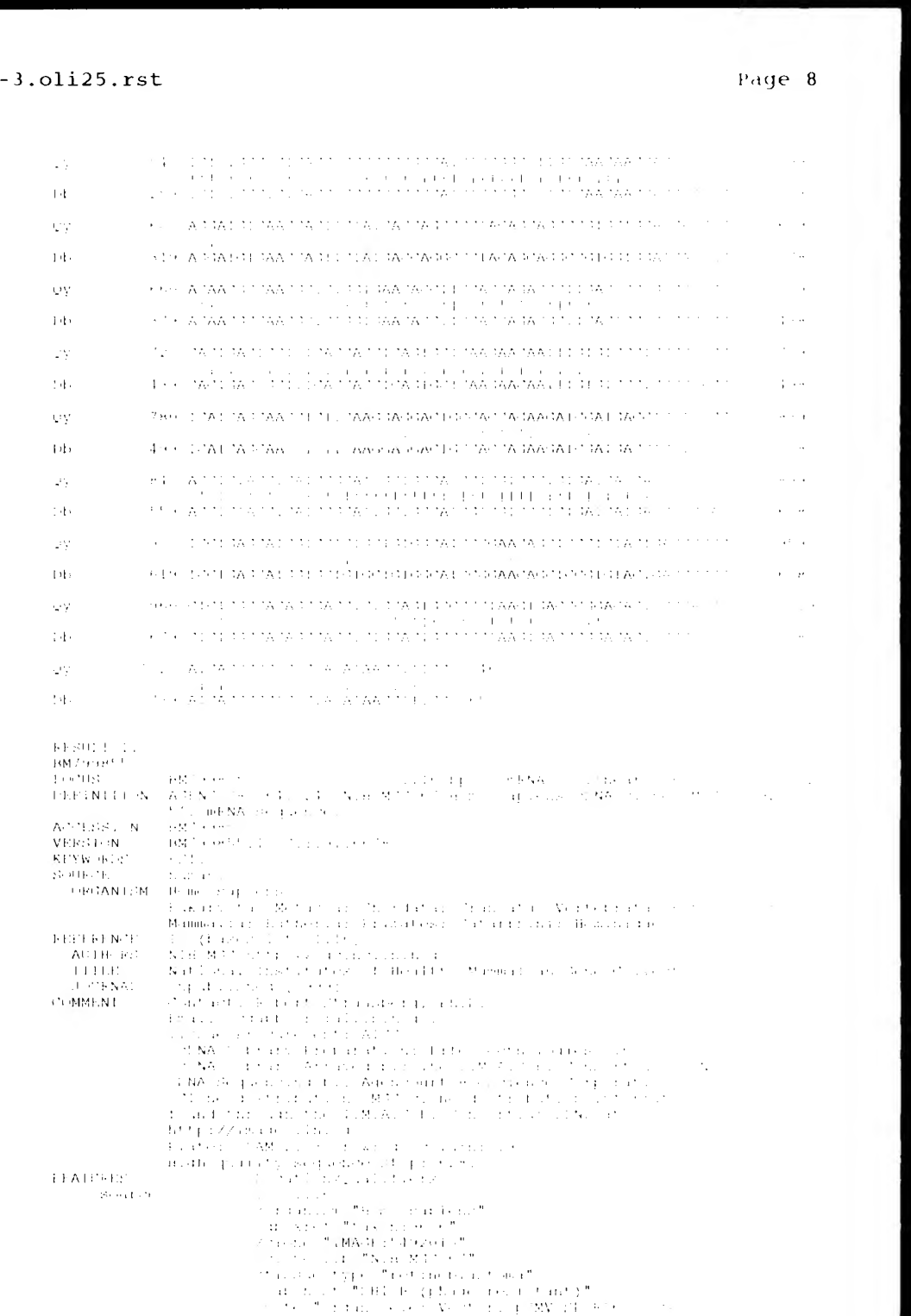

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[illegible]

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[illegible sequence alignment lines (Qy/Db), approximately 12 blocks]

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ACCESSION [illegible]
VERSION [illegible]
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE [illegible]
AUTHORS NIH MGC http://mgc.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: [illegible]
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium ([illegible])
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: [illegible] row: [illegible] column: [illegible]
High quality sequence stop: [illegible].
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. [illegible] into EcoRI/XhoI sites using the following 5' adaptor: [illegible]GCAGGAG(G). Library constructed by [illegible] laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
BASE COUNT [illegible] a [illegible] c [illegible] g [illegible] t [illegible] others
ORIGIN

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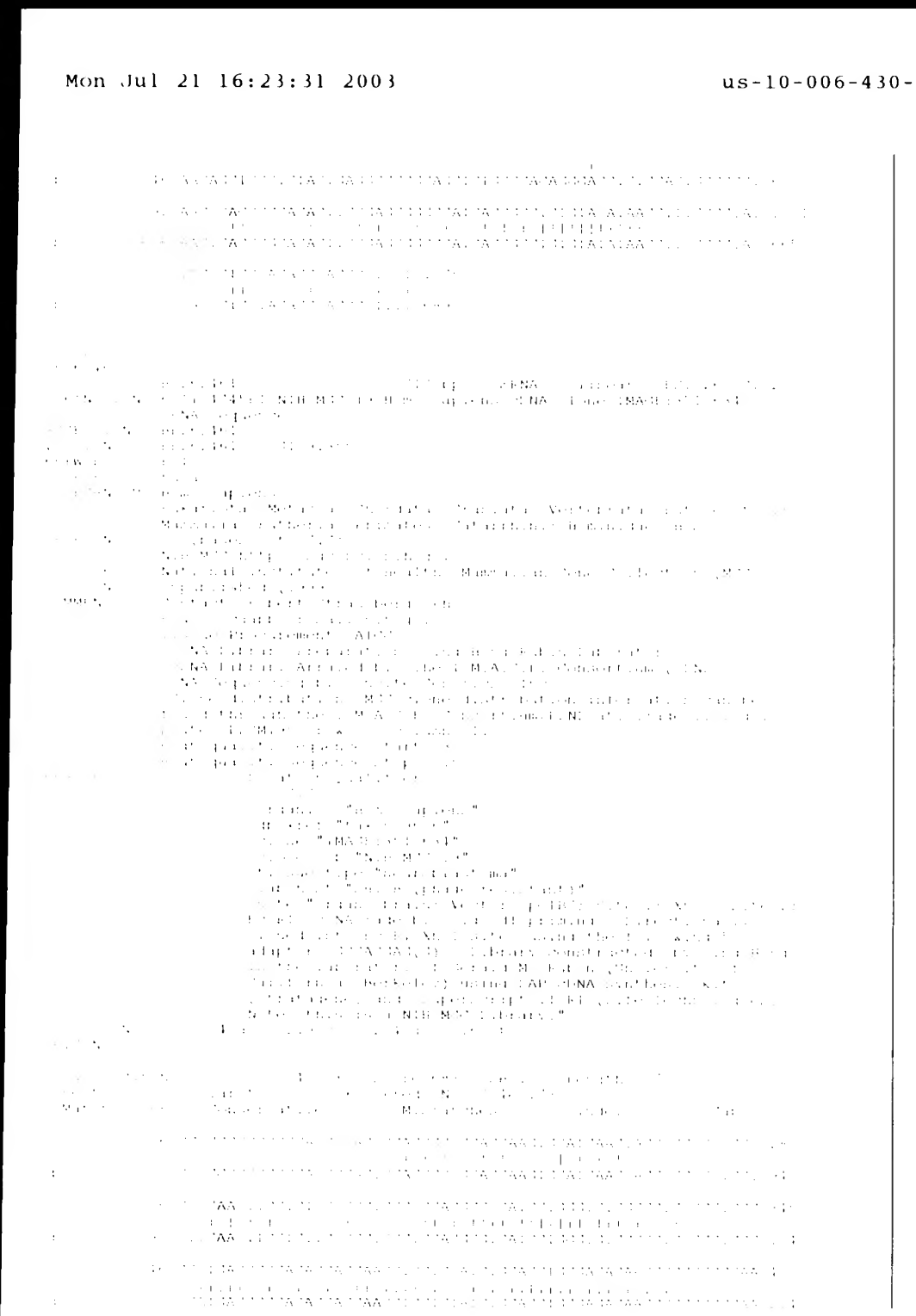
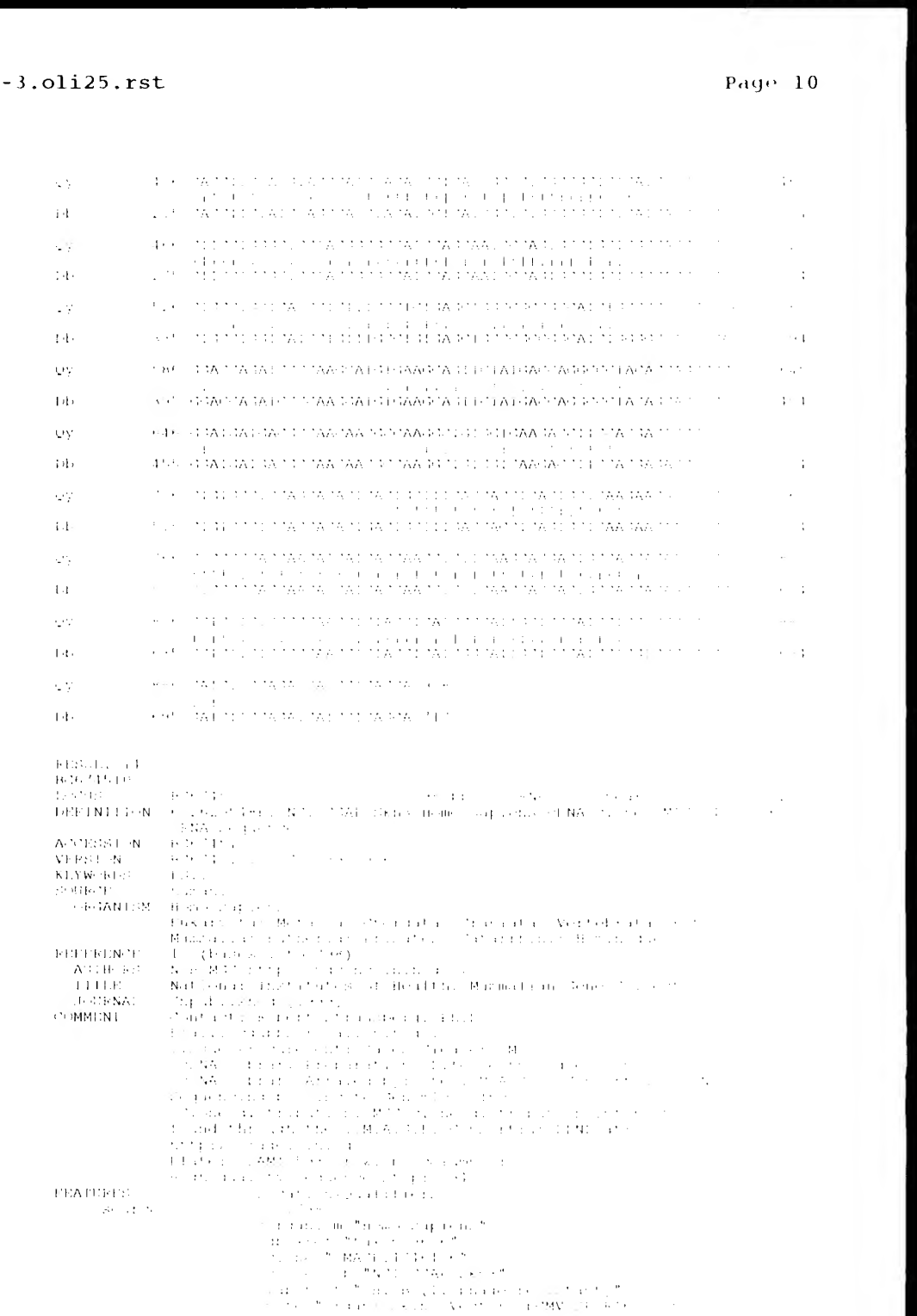
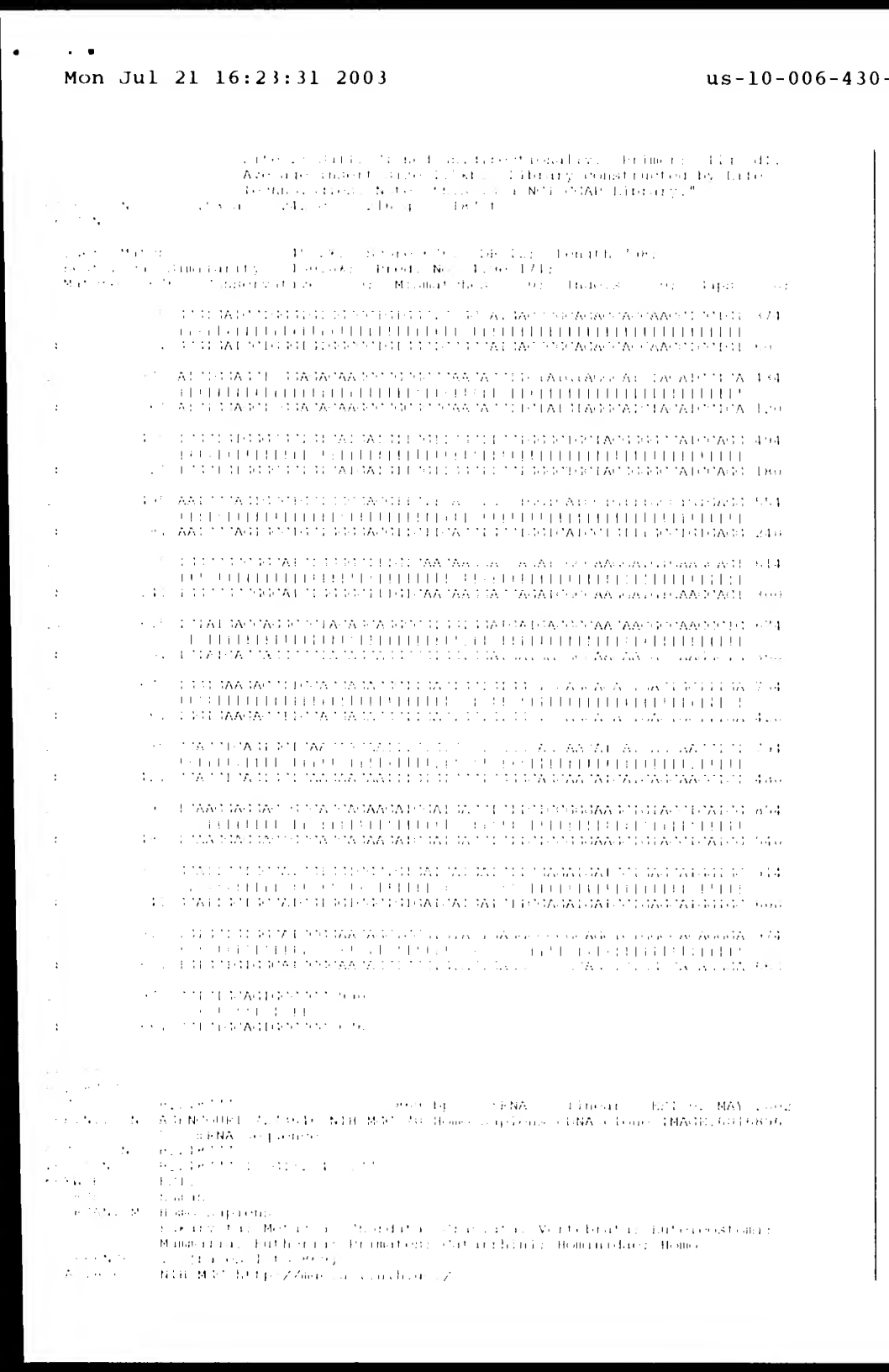
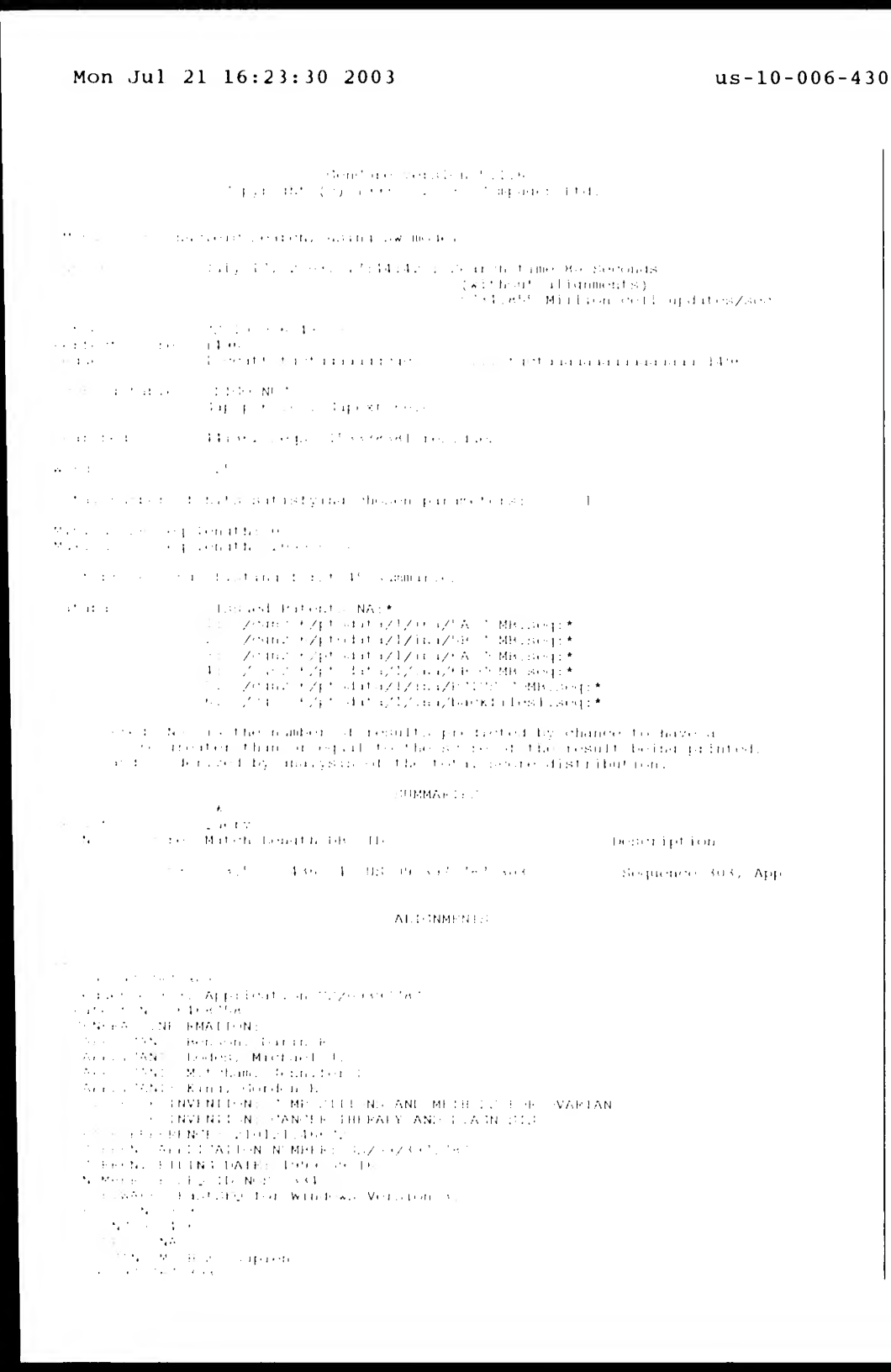
[illegible sequence alignment lines (Qy/Db), approximately 9 blocks]









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Matches [illegible] Conservative [illegible] Mismatches [illegible] Indels [illegible]

Qy [illegible]
Db [illegible]

Search completed: [illegible]
Job time : [illegible]

[illegible] nucleic search, using sw model

Run on: July 17, 2003, 18:07:37 ; Search time 350 Seconds
(without alignments)
8817.855 Million cell updates/sec

Title: US-10-006-430-3
Perfect score: 1496
Sequence: 1 ccattgtgctggaaagagc.......tgctaaaaaaaaaaaaaa 1496

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: [illegible] seqs, [illegible] residues

Word size : [illegible]

Total number of hits satisfying chosen parameters: 45

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:*
[illegible]

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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[illegible]	[illegible]	100.0	1496	15	US-10-006-[illegible]-3	Sequence 3, Appli
[illegible]	[illegible]	[illegible]	[illegible]	15	US-10-006-[illegible]-12	Sequence 12, Appl
[illegible]	[illegible]	61.6	[illegible]	10	US-09-[illegible]-21	Sequence 21, Appl
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[illegible]	[illegible]	28.3	[illegible]	12	US-09-[illegible]-12	Sequence 12, Appl
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	Result No.	Score	Query Match	Length	DB	ID	Description
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	19	278	18.6	626	15	US-10-006-430-10	[illegible]
	20	267	17.8	315	12	US-09-918-995-19449	[illegible]
c	21	189	12.6	274	11	US-09-736-457-1049	[illegible]
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c	23	189	12.6	274	11	US-09-849-626-1049	[illegible]
c	24	189	12.6	274	15	US-10-017-754-1049	[illegible]
c	25	189	12.6	275	15	US-10-102-524-98	[illegible]
c	26	176	11.8	274	11	US-09-736-457-1024	[illegible]
c	27	176	11.8	274	11	US-09-902-941-1024	[illegible]
c	28	176	11.8	274	11	US-09-849-626-1024	[illegible]
c	29	176	11.8	274	15	US-10-017-754-1024	[illegible]
c	30	173	11.6	274	11	US-09-796-692-4978	[illegible]
c	31	173	11.6	274	15	US-10-040-862-4978	[illegible]
	32	171	11.4	257	10	US-09-777-564-1383	[illegible]
	33	171	11.4	257	15	US-10-015-219-1383	[illegible]
	34	141	9.4	2994	15	US-10-027-632-114780	[illegible]
	35	101	6.8	599	15	US-10-060-036-2230	[illegible]
	36	83	5.5	311	11	US-09-920-330A-457	[illegible]
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c	42	53	3.5	249187	15	US-10-026-188-3	[illegible]
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ALIGNMENTS

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; Patent No. US20020102532A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic [illegible]
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 688290-70
; CURRENT APPLICATION NUMBER: US/09/969,708
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: [illegible]
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,608
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,125
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 132
; LENGTH: 1496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-708-132

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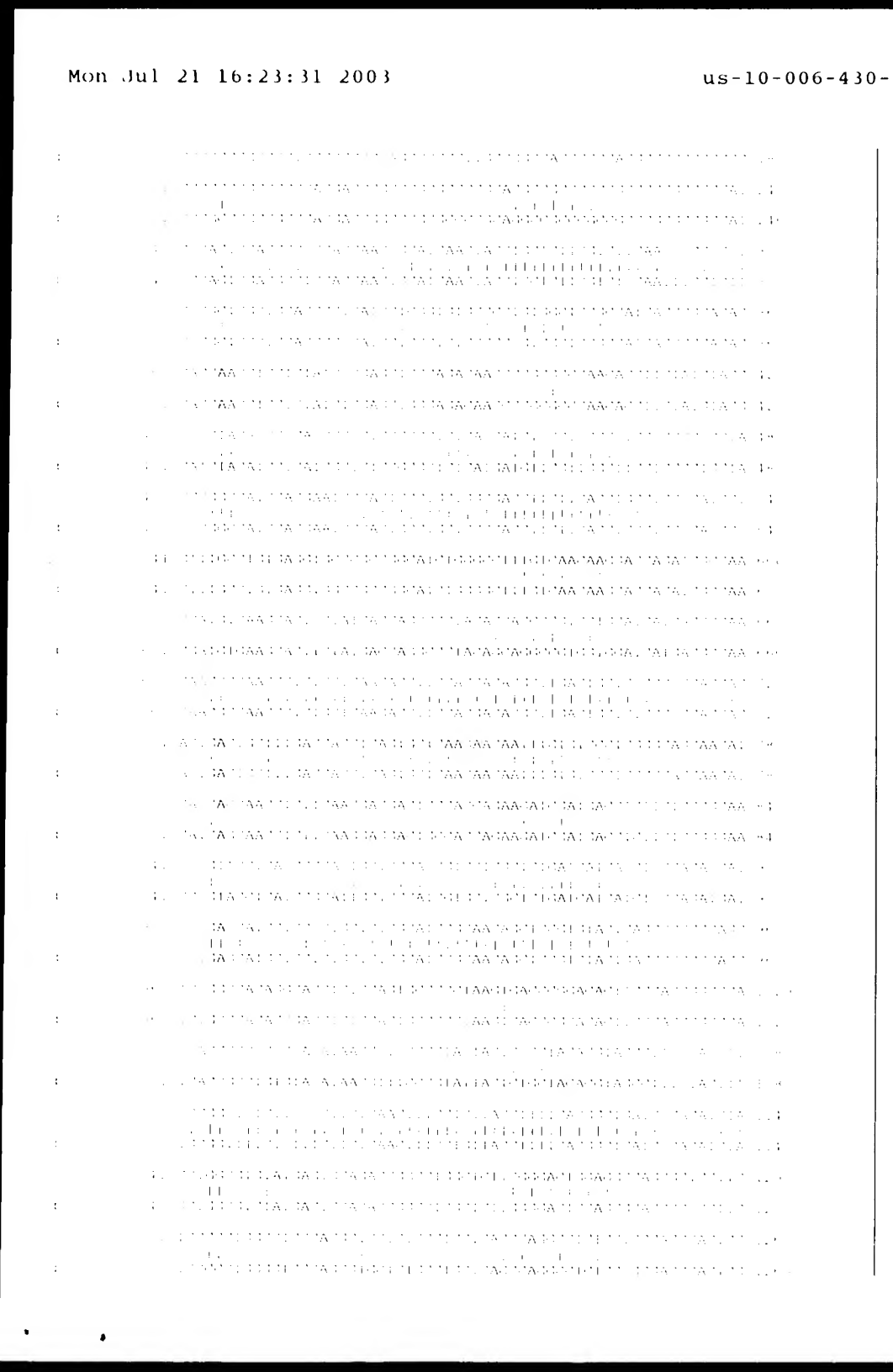

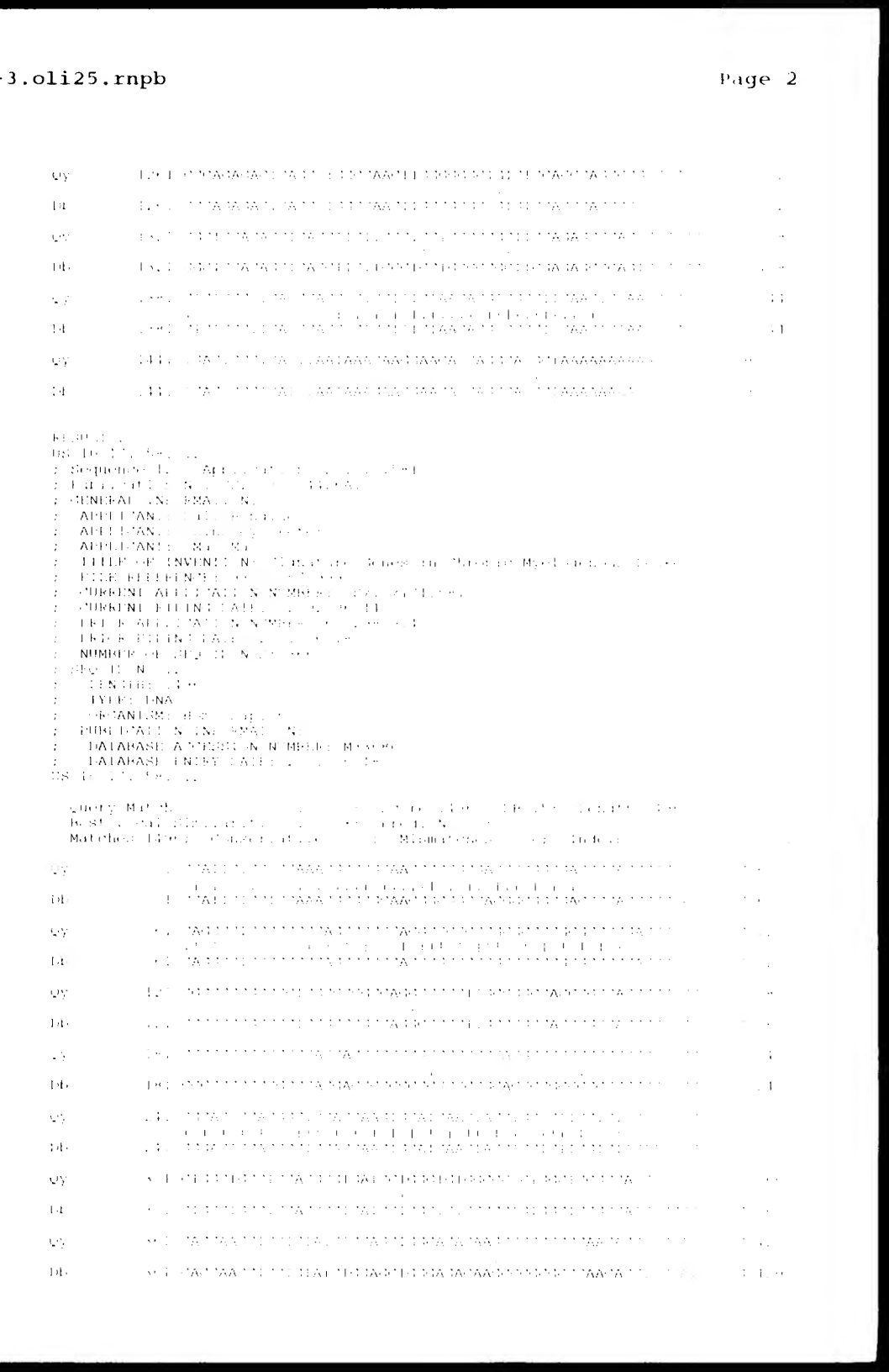

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; Publication No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Mark [illegible] Graham
;  APPLICANT: Kenneth [illegible]
;  TITLE OF INVENTION: ANTISENSE MODULATION OF [illegible] EXPRESSION
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/10/006,430
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
; SEQ ID NO [illegible]
;   LENGTH: 1496
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: ([illegible])...([illegible])
US 10-006-430-3

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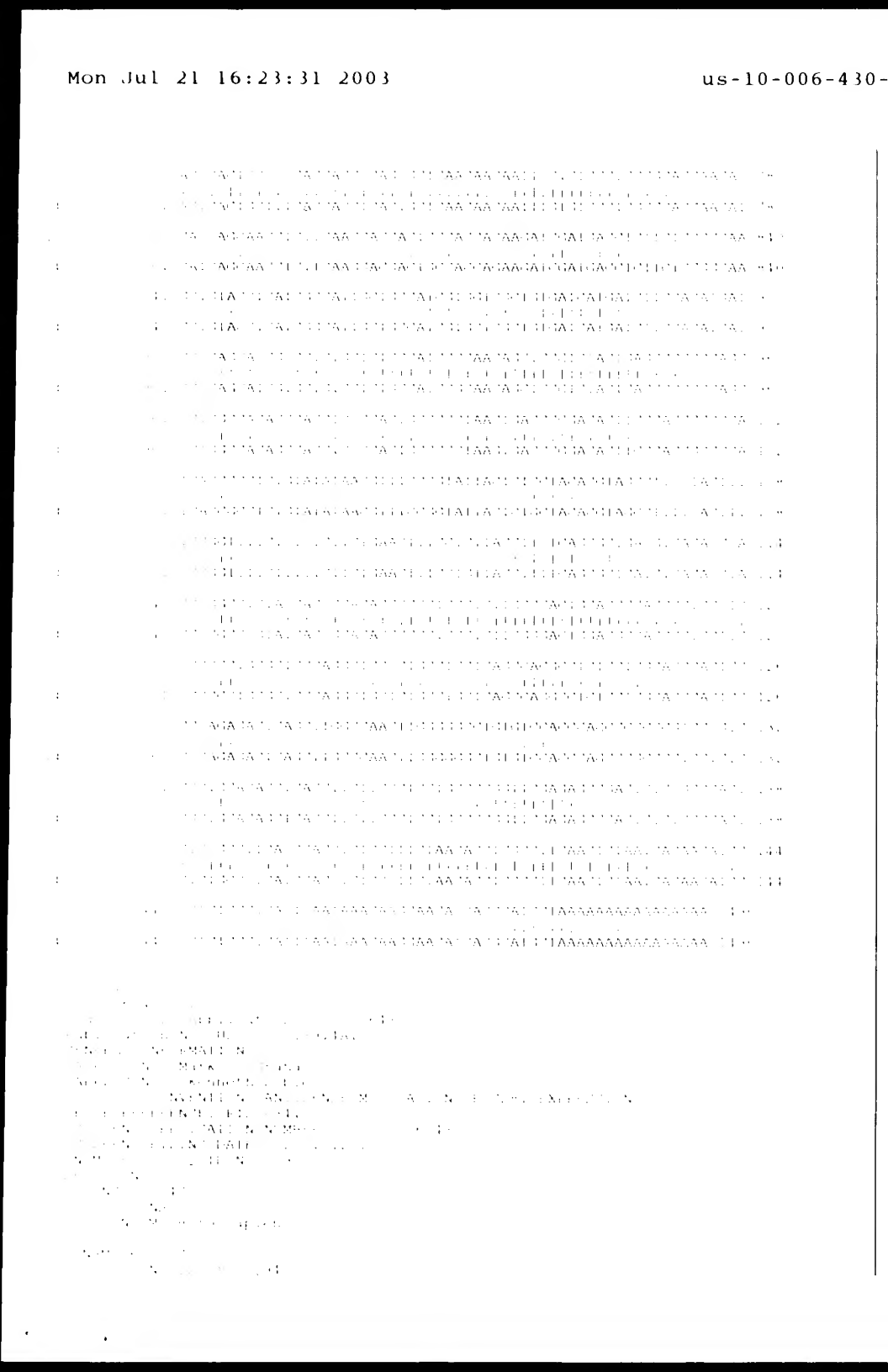

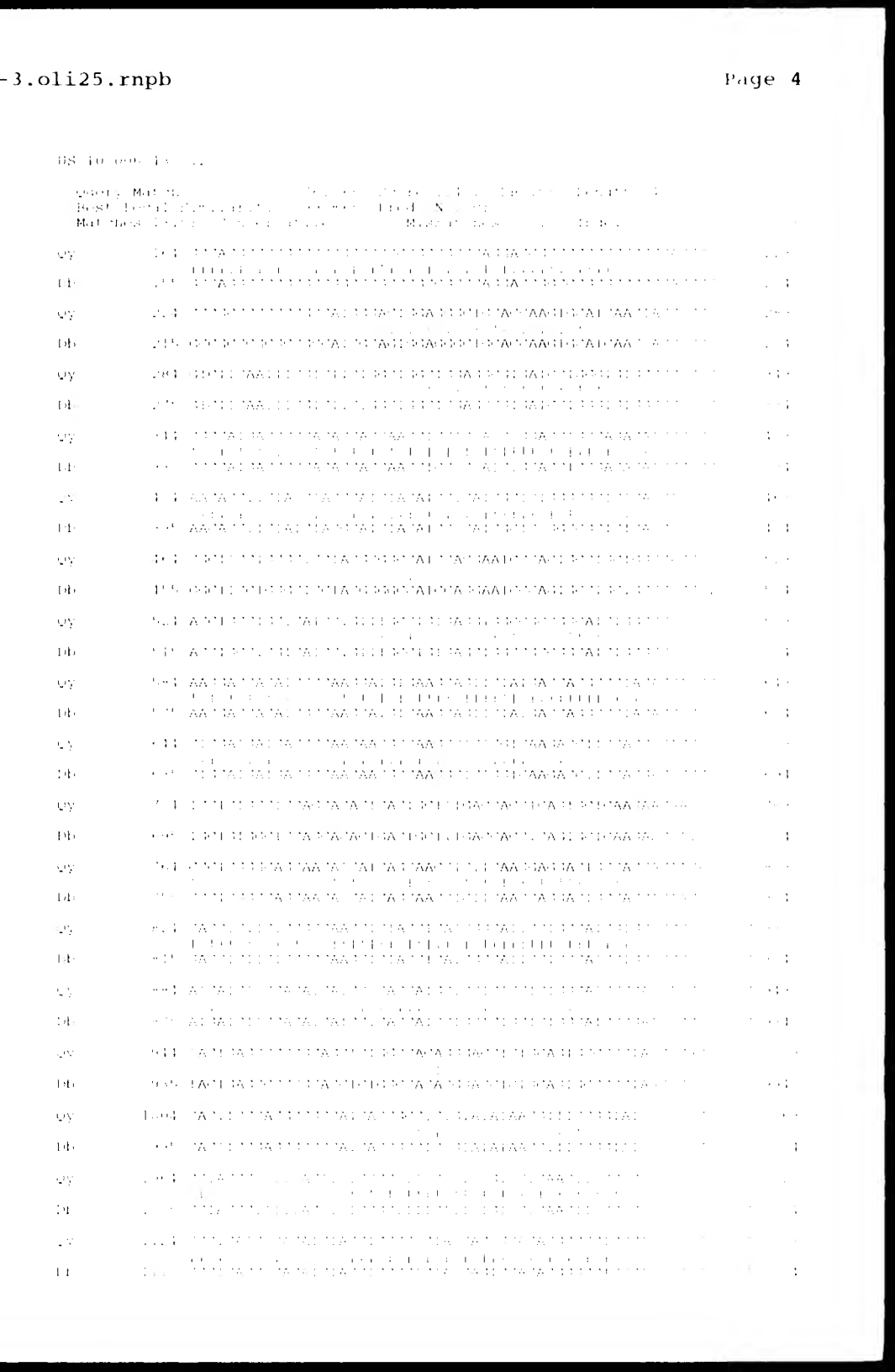

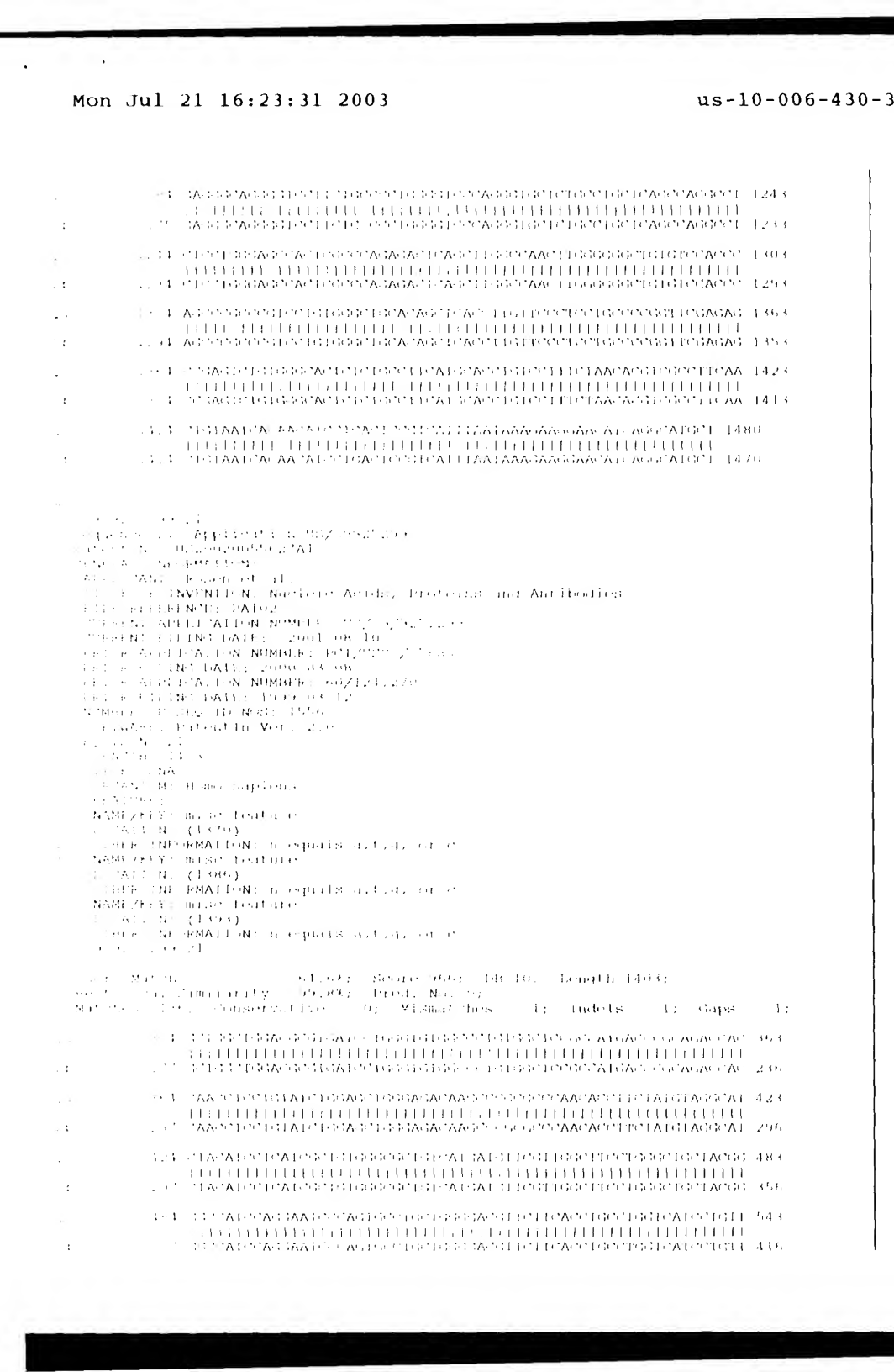

RESULT 6
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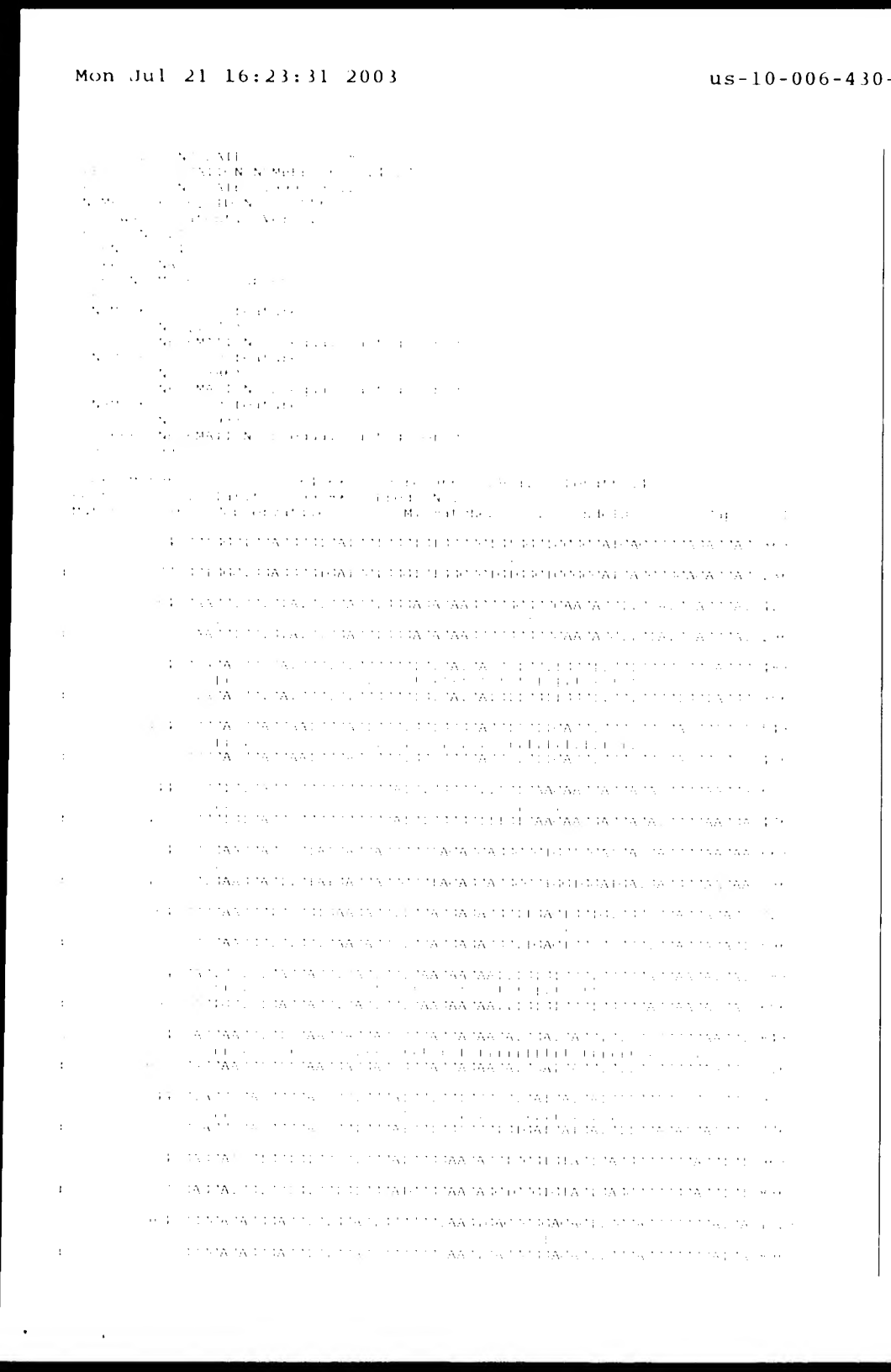
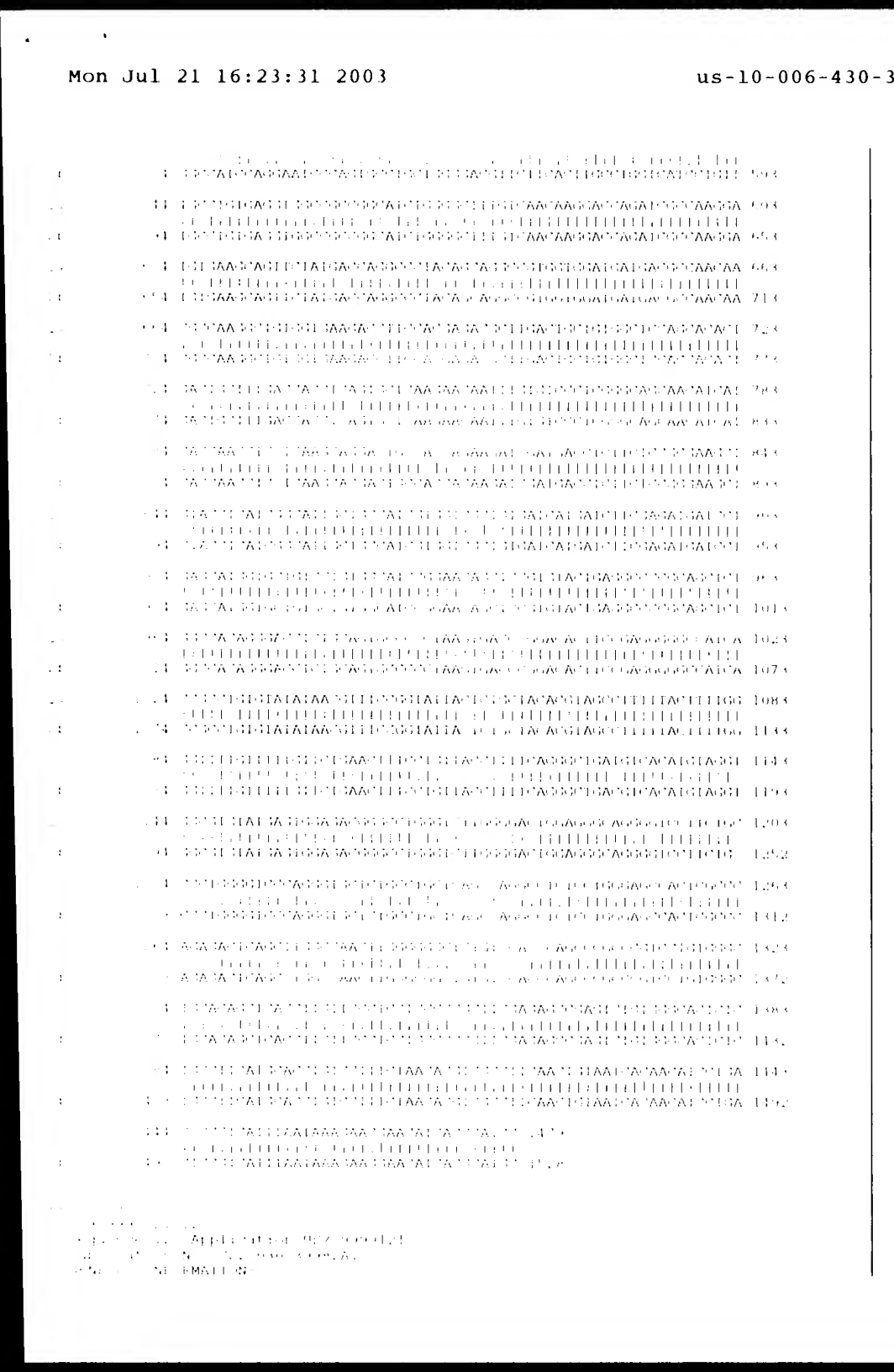
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05004





; APPLICANT: [illegible]
; TITLE OF INVENTION: ISOLATED HUMAN MET RECEPTOR TYROSINE KINASE
; TITLE OF INVENTION: HEPATOCYTE
; FILE REFERENCE: JE [illegible]
; CURRENT APPLICATION NUMBER: US/[illegible]
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/244,705
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 15540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-999-121-12

Query Match 29.8%; Score 121; DB 12; Length 15540
Best Local Similarity [illegible]; Pred. No. 5.2e-04;
Matches 594; Conservative [illegible]; Mismatches [illegible]; Indels [illegible];

RESULT 9
US-10-006-430-11
; Sequence 11, Application US/10006430
; Publication No. US2003[illegible]
; GENERAL INFORMATION:
; APPLICANT: Mark [illegible]
; APPLICANT: Kotagiri [illegible]
; TITLE OF INVENTION: ANTIBODY MEDIATED [illegible]
; FILE REFERENCE: [illegible]
; CURRENT APPLICATION NUMBER: US/[illegible]
; CURRENT FILING DATE: [illegible]
; NUMBER OF SEQ ID NOS: [illegible]